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NEWS 3 FEB 25 CA/CAPLUS - Russian Agency for Patents and Trademarks
(ROSPATENT) added to list of core patent offices covered
NEWS 4 FEB 28 PATDPAFULL - New display fields provide for legal status
data from INPADOC
NEWS 5 FEB 28 BABS - Current-awareness alerts (SDIs) available
NEWS 6 FEB 28 MEDLINE/LMEDLINE reloaded
NEWS 7 MAR 02 GBFULL: New full-text patent database on STN
NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS 9 MAR 03 MEDLINE file segment of TOXCENTER reloaded
NEWS 10 MAR 22 KOREPAT now updated monthly; patent information enhanced
NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS 12 MAR 22 PATDPASPC - New patent database available
NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS 14 APR 04 EPFULL enhanced with additional patent information and new
fields
NEWS 15 APR 04 EMBASE - Database reloaded and enhanced
NEWS 16 APR 18 New CAS Information Use Policies available online
NEWS 17 APR 25 Patent searching, including current-awareness alerts (SDIs),
based on application date in CA/CAPLUS and USPATFULL/USPAT2
may be affected by a change in filing date for U.S.
applications.
NEWS 18 APR 28 Improved searching of U.S. Patent Classifications for
U.S. patent records in CA/CAPLUS

NEWS EXPRESS JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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=> s ctggctgc/sqsn and SQL<=375
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The search profile you entered was too complex or gave too many answers. Simplify or subdivide the query and try again. If you have exceeded the answer limit, enter DELETE HISTORY at an arrow prompt (>) to remove all previous answers sets and begin at L1. Use the SAVE command to store any important profiles or answer sets before using DELETE HISTORY.

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FILE 'CAPLUS' ENTERED AT 15:41:43 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

106 L5
13008711 PY<1990
L6 0 L5 AND PY<1990

=> s 14
L7 1010 L4

=> s 17 and PY<1990
13008711 PY<1990
L8 3 L7 AND PY<1990

=> d bib ab hitstr

L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian, 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN.CNT 8

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| WO 9115771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
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| HU 62706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| HU 217025 | B | 19991129 | | |
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| JP 2733138 | B2 | 19980330 | | |
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| PL 172133 | B1 | 19970829 | PL 1991-296329 | 19910329 |
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| AT 182684 | E | 19990815 | AT 1995-114016 | 19910403 |
| ES 2134388 | T3 | 19991001 | ES 1995-114016 | 19910403 |
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| NO 310241 | B1 | 20010611 | | |
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| LV 10306 | B | 19950620 | LV 1993-442 | 19930531 |
| LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
| US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |
| US 5350671 | A | 19940927 | US 1993-103961 | 19930809 |

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| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
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| US 6074816 | A | 20000613 | US 1994-307273 | 19940916 |
| US 5712087 | A | 19980127 | US 1995-440519 | 19950512 |
| US 6312889 | B1 | 20011106 | US 1995-440549 | 19950512 |
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| US 6096541 | A | 20000801 | US 1995-441026 | 19950515 |
| US 6171782 | B1 | 20010109 | US 1995-442647 | 19950515 |
| US 6861212 | B1 | 20050301 | US 1995-441355 | 19950515 |
| US 5863719 | A | 19990126 | US 1995-472821 | 19950607 |
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| NO 303879 | B1 | 19980914 | | |
| US 2003162167 | A1 | 20030828 | US 1996-686983 | 19960725 |
| JP 09173079 | A2 | 19970708 | JP 1996-241451 | 19960822 |
| JP 3171793 | B2 | 20010604 | | |
| FI 9801380 | A | 19980615 | FI 1998-1380 | 19980615 |
| FI 106564 | B1 | 20010228 | | |
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| US 1987-139886 | A | 19871230 | | |
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| US 1988-191263 | A | 19880506 | | |
| US 1988-263584 | A | 19881026 | | |
| US 1988-271450 | A | 19881114 | | |
| CN 1988-107988 | A | 19881118 | | |
| JP 1992-361785 | A3 | 19881118 | | |
| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
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| JP 1998-111631 | A3 | 19881118 | | |
| WO 1988-US4125 | A | 19881118 | | |
| YU 1988-2138 | A6 | 19881118 | | |
| US 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353896 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
| US 1989-355961 | B2 | 19890518 | | |
| NO 1989-2931 | A | 19890717 | | |
| US 1989-398667 | B2 | 19890825 | | |
| US 1989-456637 | B2 | 19891221 | | |
| US 1990-504352 | A | 19900404 | | |
| US 1990-505435 | B2 | 19900404 | | |
| US 1990-566209 | B1 | 19900808 | | |
| US 1990-611965 | B2 | 19901108 | | |
| WO 1991-US2225 | A | 19910329 | | |
| EP 1991-302910 | A3 | 19910403 | | |
| US 1992-910760 | A3 | 19920707 | | |
| US 1993-40564 | A3 | 19930331 | | |
| US 1993-103961 | A1 | 19930809 | | |
| US 1994-306472 | A3 | 19940915 | | |
| US 1994-307273 | A3 | 19940916 | | |

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated

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from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

=> d bib ab seq 1-3
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CBIB ----- AN, plus Compressed Bibliographic Data
DALL ----- ALL, delimited (end of each field identified)
DMAX ----- MAX, delimited for post-processing
FAM ----- AN, PI and PRAI in table, plus Patent Family data
FBIB ----- AN, BIB, plus Patent FAM
IND ----- Indexing data
IPC ----- International Patent Classifications
MAX ----- ALL, plus Patent FAM, RE
PAT5 ----- PI, SO.
SAM ----- CC, SX, TI, ST, IT
SCAN ----- CC, SX, TI, ST, IT (random display, no answer numbers;
SCAN must be entered on the same line as the DISPLAY,
e.g., D SCAN or DISPLAY SCAN)
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IALL ----- ALL, indented with text labels
IBIB ----- BIB, indented with text labels
IMAX ----- MAX, indented with text labels
ISTD ----- STD, indented with text labels

OBIB ----- AN, plus Bibliographic Data (original)
OIBIB ----- OBIB, indented with text labels

SBIB ----- BIB, no citations
SIBIB ----- IBIB, no citations

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HITIND ----- IC, ICA, ICI, NCL, CC and index field (ST and IT)
containing hit terms
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HITSTR ----- HIT RN, its text modification, its CA index name, and
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HITSEQ ----- HIT RN, its text modification, its CA index name, its
structure diagram, plus NTE and SEQ fields
FHITSTR ----- First HIT RN, its text modification, its CA index name, and

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its structure diagram
 FHITSEQ ----- First HIT RN, its text modification, its CA index name, its structure diagram, plus NTE and SEQ fields
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 OCC ----- Number of occurrence of hit term and field in which it occurs

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L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
 DN 120:296653
 TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
 IN Houghton, Michael; Choo, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian, 157 pp.
 CODEN: INXXAP
 DT Patent
 LA English

FAN.CNT 8

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| JP 1992-361785 | A3 | 19881118 |
| JP 1992-361787 | A3 | 19881118 |
| JP 1993-178446 | A3 | 19881118 |
| JP 1996-241451 | A3 | 19881118 |
| JP 1998-111631 | A3 | 19881118 |
| WO 1988-US4125 | A | 19881118 |
| YU 1988-2138 | A6 | 19881118 |
| US 1989-325338 | B2 | 19890317 |
| US 1989-341334 | B2 | 19890420 |
| US 1989-353896 | B2 | 19890421 |
| US 1989-355002 | B2 | 19890518 |
| US 1989-355961 | B2 | 19890518 |
| NO 1989-2931 | A | 19890717 |
| US 1989-398667 | B2 | 19890825 |
| US 1989-456637 | B2 | 19891221 |
| US 1990-504352 | A | 19900404 |
| US 1990-505435 | B2 | 19900404 |
| US 1990-566209 | B1 | 19900808 |
| US 1990-611965 | B2 | 19901108 |
| WO 1991-US2225 | A | 19910329 |
| EP 1991-302910 | A3 | 19910403 |
| US 1992-910760 | A3 | 19920707 |
| US 1993-40564 | A3 | 19930331 |
| US 1993-103961 | A1 | 19930809 |
| US 1994-306472 | A3 | 19940915 |
| US 1994-307273 | A3 | 19940916 |

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgcgt ggcatagtg ggcagggtcg tcttgtccgg gaagccggca
51 atcataacctg acatggaaatg cctctaccga gagttcgatg agatggaaaga
101 gtgctctcg cacttaccgt acatcgagca aaggatgtatg ctcgcccggc
151 agttcaagca gaaggccctc ggcctcctgc agaccgcgtc ccgtcaggca
201 gaggttatcg cccctgtgtt ccagaccaac tggaaaaac tcgagacatt
251 ctggcgaag catatgtgga acttcatcg tggataca tacttggcg
301 gcttgtaac gtcgcctggt aaccccgcca ttgcttcatt gatggcttt
351 acagctgctg tcaccagccc actaaccact agccaaa

STN Columbus

AN 1989:401656 CAPLUS
DN 111:1656
TI The sequence of hemC, hemD and two additional E. coli genes
AU Alefounder, Peter R.; Abell, Chris; Battersby, Alan R.
CS Chem. Lab., Univ. Cambridge, Cambridge, BCB2 1EW, Guatemala
SO Nucleic Acids Research (1988), 16(20), 9871
=====
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A 4260-bp sequence from Escherichia coli contg. the porphobilinogen deaminase gene hemC, the uroporphyrinogen III cosynthetase gene hemD plus 2 moré genes X and Y is presented. Genes hemC, hemD, and X are all part of the Uro operon.
IT 104708-82-9, Deoxyribonucleic acid (Escherichia coli clone pLC41-4 gene hemC)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)
RN 104708-82-9 CAPLUS
CN DNA (Escherichia coli clone pLC41-4 gene hemC) (9CI) (CA INDEX NAME)
NTE doublestranded

SEQ 1 atgttagaca atgttttaag aattgccaca cgccaaagcc cacttgcact
 51 ctggcaggca cactatgtca aagacaagtt gatggcgagc catccgggcc
 101 tggtcgttga actggtaccc atggtgacgc gggcgatgt gattcttgc
 151 acgccgctgg cgaaaagtgg cggaaaaggc ttattttaa aagagctgga
 201 agtcgcgtc ctgaaaatc ggcgcgatat cgccgtacac tcaatgaaag
 251 atgtgcgggt tgaattcccg caaggtctgg gactggtcac tatttgcgg
 301 cgtgaagatc ctcgcgtatgc ctttgcgtcc aataactatg acagtctgga
 351 tgcgttaccg gcaggcgtta tcgtcgggac gtccagttt cgtcgccagt
 401 gccaactggc tgaacgcgtt ccggatctga ttatccgctc cctgcgcggc
 451 aacgtcggca ctgcgttgcg caaactggat aacggcgaat acgtgcgt
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 601 gtgggttattt aatggccgtt tgatgattca cgcactcgat agctgttgc
 651 cgcgttgcgtt caccacggaa ctgcgttgcg cggttaccgca gaacgcgc
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 851 aacaaatggg gatttcgttgcg tcgttgcgttgcgatgatgc
 901 gagatcctcg ctgttgcgttgcgatgatgc gccccggcat ga

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:565982 CAPLUS
DN 105:165982
TI Nucleotide sequence of the hemC locus encoding porphobilinogen deaminase of Escherichia coli K12
AU Thomas, Steven D.; Jordan, Peter M.
CS Dep. Biochem., Univ. Southampton, Southampton, SO9 3TU, UK
SO Nucleic Acids Research (1986), 14(15), 6215-26
=====
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Porphobilinogen deaminase [9074-91-3], the product of the hemC locus in E. coli K12, catalyzes the tetrapolymer of porphobilinogen (PBG) into the hydroxymethylbilane, preuroporphyrinogen. The hemC locus was subcloned

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from the Clarke and Carbon plasmid pLC41-4. The sequence of the hemC structural gene and flanking DNA was detd. by the dideoxy chain-termination method of Sanger. The structural gene for hemC is located within a 942-base-pair sequence encoding the monomeric PBG deaminase, mol. wt. 33,857. The extent of the coding region was confirmed by sequencing the N-terminus of the purified enzyme and by detn. of the mol. wt. The hemC locus is closely linked to the cyaA locus, the genes being transcribed in a divergent manner. Upstream of the hemC coding region, a possible promoter and 3 repeated GGATG sequences were identified. This is the 1st report of a complete DNA sequence for a structural gene specifying an enzyme of the heme biosynthetic pathway in prokaryotes.

IT 104708-82-9

RL: FRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 104708-82-9 CAPLUS

CN DNA (Escherichia coli clone pLC41-4 gene hemC) (9CI) (CA INDEX NAME)

NTE doublestranded

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101 tggctgtga actggtacccg atggtgacgc gggcgatgt gattcttgat
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201 ag:cgcgctc ctcgaaaatc gcgcgcgatat cgccgtacac tcaatgaag
251 atgtgcgggt tgaattcccg caaggtctgg gactggtcac tatttgtgag
301 cgtgaagatc ctcgcgtatgc ctttgttgc aataactatg acagtctgga
351 tgcgttaccg gcaggcgatgta tcgtcgggac gtccagttt cgtcgccagt
401 gccaactggc tgaacgcgtt ccggatctga ttatccgctc cctgcgcggc
451 gagctcggtca ctcgcctgag caaactggat aacggcgaat acgatggcat
501 catttttgcc ttagccggac taaaacgttt aggtctggag tcacgtattc
551 tgccgcgtt gccacccgag atttcttcc cggcggtagg acaaggtgctg
601 ggggttattt aatgccgcct tggatgatca cgcactcgcg agctgttgc
651 cggcggtgtaa caccacgaaa ctgcactcgcg cttaccgca gaacgcgc
701 tggatgttaccgg tctcgttggc gcatgttgcagg tgccatttgg tagctacggc
751 gagtttttattt atggcgaaat ctggctgcgtt gggctggctg ggcgcgcgg
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851 Aactttatggg gatttcgttgc gcaagaagagc tactgtataa cggcgccgc
901 cggatccctcg ctgttggatca taacggagac gccccggcat ga |
|-----|--|

u.s. 15

1.9 106 35

=> is 15 and PY<1991

206 L5

13523241 PY<1991

1.10 9 LS AND PY<1991

=> s_19 and PY<1991

13523241 PY<1991

L11 0- L9 AND PY<1991

=> file registry

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|---------------------|-------|---------|
| CA SUBSCRIBER PRICE | -2.92 | -2.92 |

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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=> s tcaccagccc/sqsn
L13      78505 TCACCAGCCC/SQSN

=> file caplus
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FULL ESTIMATED COST          35.21         127.26

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                                              ENTRY        SESSION
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L14 7141 L13

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L15 64 L14 AND PY<1990

=> d bib ab hitseq

L15 ANSWER 1 OF 64 CAPLUS CCOPYRIGHT 2005 ACS on STN

Full Text:

AN 1996:702025 CAPLUS
DN 125:58966
TI DNA encoding various truncated and mutein forms of human and murine colony stimulating factor-1
IN Ladner, Martha B.; Noble, Janelle A.; Martin, George A.; Kawasaki, Ernest S.; Coyne, Mazie Y.; Halenbeck, Robert F.; Koths, Kirston E.
PA Cetus Oncology Corp., USA
SO U.S., 45 pp.. Cont.-in-part of U.S. Ser. No. 799, 039, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------|------|----------|-----------------|--------------|
| US 5573930 | A | 19961112 | US 1992-999298 | 19921228 |
| CA 1339873 | A1 | 19980519 | CA 1986-500902 | 19860131 |
| ES 551665 | A1 | 19870301 | ES 1986-551665 | 19860205 <-- |
| ZA 8600839 | A | 19871028 | ZA 1986-839 | 19860205 <-- |
| ZA 9707979 | A | 19890628 | ZA 1987-7979 | 19871023 <-- |
| AT 105869 | E | 19940615 | AT 1987-309409 | 19871023 |
| IL 34257 | A1 | 19970218 | IL 1987-84257 | 19871023 |
| US 4847201 | A | 19890711 | US 1988-157094 | 19880209 <-- |
| US 5470569 | A | 19951128 | US 1994-212300 | 19940314 |
| US 5556620 | A | 19960917 | US 1994-220454 | 19940331 |
| US 5614183 | A | 19970325 | US 1995-371803 | 19950111 |
| US 5635175 | A | 19970603 | US 1995-371804 | 19950111 |
| US 5837229 | A | 19981117 | US 1995-371805 | 19950111 |
| US 5681719 | A | 19971028 | US 1995-401013 | 19950308 |
| US 6204020 | 31 | 20010320 | US 1995-401632 | 19950309 |
| US 5643563 | A | 19970701 | US 1995-426036 | 19950421 |
| US 5672343 | A | 19970930 | US 1995-426279 | 19950421 |
| US 6103224 | A | 20000815 | US 1995-426570 | 19950421 |
| US 6117422 | A | 20000912 | US 1995-425876 | 19950421 |
| US 6146851 | A | 20001114 | US 1995-426243 | 19950421 |

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| | | | | |
|---------------------|----|----------|----------------|----------|
| US 6156300 | A | 20001205 | US 1995-426571 | 19950421 |
| PRAI US 1985-698359 | B2 | 19850205 | | |
| US 1985-728834 | B2 | 19850430 | | |
| US 1985-744924 | B2 | 19850614 | | |
| US 1985-756814 | B2 | 19850718 | | |
| US 1986-821068 | B2 | 19860121 | | |
| US 1986-876819 | B2 | 19860620 | | |
| US 1986-923067 | B2 | 19861024 | | |
| US 1987-39654 | B2 | 19870416 | | |
| US 1987-39657 | B1 | 19870416 | | |
| US 1987-105261 | B2 | 19871013 | | |
| US 1991-799039 | B2 | 19911127 | | |
| US 1991-799411 | B2 | 19911127 | | |
| US 1987-99872 | A2 | 19870922 | | |
| EP 1987-309409 | A | 19871023 | | |
| US 1988-157094 | A3 | 19880209 | | |
| US 1988-243253 | B2 | 19880914 | | |
| US 1989-358394 | B1 | 19890526 | | |
| US 1990-505256 | B1 | 19900405 | | |
| US 1991-794822 | B1 | 19911118 | | |
| US 1992-999280 | A3 | 19921228 | | |
| US 1993-24094 | B1 | 19930226 | | |
| US 1994-220454 | A3 | 19940331 | | |
| US 1995-401632 | A3 | 19950309 | | |

AB A colony stimulating factor, CSF-1, is a lymphokine useful in regulating the immune system is a lymphokine useful in overcoming the immunosuppression induced by chemotherapy or resulting from other causes. CSF-1 is obtained in usable amts. by recombinant methods, including cloning and expression of the murine and human DNA sequences encoding this protein. Both long and short forms of the human protein and muteins corresponding to the cDNA-encoded forms are disclosed. Thus, deletion of the first 3 N-terminal residues (Glu-Glu-Val) of mature CSF-1 (NV3) yields constructs that are expressed in Escherichia coli with ~95% of the N-terminal methionines removed. C-terminal truncated derivs. were also prep'd., with the new C-terminal residue at the 150, 190, 191, 221, 223, 234, 238, 249, 250, 258 or 411 positions. Muteins encoding an Asp at residue 59 (preferably via a GAT codon) do not show an internal restart translation product, thereby removing one cause of heterogeneity. Addnl. muteins can include substitution of lysine-52 with a glutamine residue, alteration of one or more glycosylation sites, and the cysteine-90 residue is dispensable to immunoreactivity. The CSF-1 proteins are capable both of stimulating monocyte-precursor/macrophage cell prodn. from progenitor cells, thus enhancing the effectiveness of the immune system, and of stimulating the functions of these differentiated cells as the secretion of lymphokines in the mature macrophages. They are also useful anti-infective agents, esp. as antiviral and antimicrobial agents.

IT 117277-07-3DP, N- and C-terminal truncated and substituted muteins
 117277-09-5DP, N- and C-terminal truncated and substituted muteins
 RI: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (nucleotide sequence; DNA encoding various truncated and mutein forms
 of human and murine colony stimulating factor-1)

PN 117277-07-3 CAPLUS
 CN (mouse clone pcDBmuCSF-L colony-stimulating factor 1 cDNA plus flanks) (PCI) (CA INDEX NAME)

SSQ 1 tgaaagtttg cctcggtgtc ctgcggctct ctgcatccca
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251 ttggcaagga ggtgtcagaa cactgttagcc acatgatttg gaatggacac
301 ctgaaggctcc tgacgcaggat gatcgacagt caaatggaga cttcatgcca
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401 acctaaagaa ggcctttttt ctggtacaag acataataga tgagaccatg
451 cgctttaaag acaacacccc caatgtaac gccaccgaga ggctccagga
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601 aagatcaaga acttctttaa tgaaaacaag aatctcttg aaaaggactg
651 gaacatfffft accaagaact gcaacaacag cttgctaag tgctctagcc
701 gagatgttgtt gaccaagctt gattgcaact gcctgtaccc taaagccacc
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RN 117277-09-5 CAPLUS
CN DNA, (mouse clone pcDBmuCSF-S colony-stimulating factor 1 cDNA plus flanks) (9CI) (CA INDEX NAME)

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1001 ctatgtgggg atttttgcac caggaagcaa agttttcccc ctccacgcct
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1251 ccaggagcc ggtcttcccc atattgcac accgaatccc caacgagtca
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STN Columbus

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| FULL ESTIMATED COST | 10.29 | 137.55 | |
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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* The CA role and document type information have been removed from *
* the IDR default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter 'HELP PROP' at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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227 3436 SQL<400
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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L17 1318 L16

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L18 2 L17 AND PY<1990

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L18 ANSWER OF 2 CAPLUS COPYRIGHT 2005 ACS ON STN

Full Text

AN 1990-255653 CAPLUS

DN 12008711

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Hougaard, Michael; Choo, Qui Lim; Kuo, George

PA Chirurg Corp., India

SO Indian. 157 pp.

CODEN INXXAP

DT Patent

LA English

FAN.CNT 2

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| JP 05081600 | B4 | 19931115 | JP 1989-500565 | 19881118 |
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STN Columbus

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| WO 9115771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
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| BR 9106309 | A | 19930420 | BR 1991-6309 | 19910329 |
| HU 62706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| HU 217025 | B | 19991129 | | |
| JP 05508219 | T2 | 19931118 | JP 1991-507636 | 19910329 |
| JF 2733138 | B2 | 19980330 | | |
| RC 109916 | B1 | 19950728 | RO 1975-92012 | 19910329 |
| PL 172133 | B1 | 19970829 | PL 1991-296329 | 19910329 |
| RU 2130969 | C1 | 19990527 | RU 1991-5053084 | 19910329 |
| EP 450931 | A1 | 19911009 | EP 1991-302910 | 19910403 |
| EP 450931 | B1 | 19960612 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| EP 693687 | A1 | 19960124 | EP 1995-114016 | 19910403 |
| EP 693687 | B1 | 19990728 | | |
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| ES 2088465 | T3 | 19960816 | ES 1991-302910 | 19910403 |
| AT 182684 | E | 19990815 | AT 1995-114016 | 19910403 |
| ES 2134388 | T3 | 19991001 | ES 1995-114016 | 19910403 |
| US 5682664 | A | 19971104 | US 1992-910760 | 19920707 |
| FI 106317 | B1 | 20010115 | FI 1992-4349 | 19920928 |
| NO 9203839 | A | 19921119 | NO 1992-3839 | 19921001 |
| NO 310241 | B1 | 20010611 | | |
| US 5714596 | A | 19980203 | US 1993-40564 | 19930331 |
| LV 10306 | B | 19950620 | LV 1993-442 | 19930531 |
| LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
| US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |
| US 5350671 | A | 19940927 | US 1993-103961 | 19930809 |
| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
| HR 940493 | B1 | 20001031 | HR 1994-940493 | 19940907 |
| US 5698390 | A | 19971216 | US 1994-306472 | 19940915 |
| US 6074816 | A | 20000613 | US 1994-307273 | 19940916 |
| US 5712087 | A | 19980127 | US 1995-440519 | 19950512 |
| US 6312889 | B1 | 20011106 | US 1995-440549 | 19950512 |
| US 5712088 | A | 19980127 | US 1995-440769 | 19950515 |
| US 6096541 | A | 20000801 | US 1995-441026 | 19950515 |
| US 6171782 | B1 | 20010109 | US 1995-442647 | 19950515 |
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| US 5863719 | A | 19990126 | US 1995-472821 | 19950607 |
| NO 9505101 | A | 19951215 | NO 1995-5101 | 19951215 |
| NC 306511 | B1 | 19991115 | | |
| NO 9505102 | A | 19951215 | NO 1995-5102 | 19951215 |
| NO 303879 | B1 | 19980914 | | |
| US 2003162167 | A1 | 20030828 | US 1996-686983 | 19960725 |

STN Columbus

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| JP 09173079 | A2 | 19970708 | JP 1996-241451 | 19960822 |
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| GR 3031361 | T3 | 20000131 | GR 1999-402455 | 19990929 |
| PRAI US 1987-122714 | A | 19871118 | | |
| IN 1983-CA960 | A | 19881118 | | |
| US 1987-139886 | A | 19871230 | | |
| US 1988-161072 | A | 19880226 | | |
| US 1988-191263 | A | 19880506 | | |
| US 1988-263584 | A | 19881026 | | |
| US 1988-271450 | A | 19881114 | | |
| CN 1988-107988 | A | 19881118 | | |
| JP 1992-361785 | A3 | 19881118 | | |
| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
| JP 1996-241451 | A3 | 19881118 | | |
| JP 1998-111631 | A3 | 19881118 | | |
| WO 1988-US4125 | A | 19881118 | | |
| YU 1988-2138 | A6 | 19881118 | | |
| US 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353896 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
| US 1989-355961 | B2 | 19890518 | | |
| NO 1989-2931 | A | 19890717 | | |
| US 1989-398667 | B2 | 19890825 | | |
| US 1989-456637 | B2 | 19891221 | | |
| US 1990-504352 | A | 19900404 | | |
| US 1990-505435 | B2 | 19900404 | | |
| US 1990-566209 | B1 | 19900808 | | |
| US 1990-611965 | B2 | 19901108 | | |
| US 1991-US2225 | A | 19910329 | | |
| EP 0291-302910 | A3 | 19910403 | | |
| EP 0981-910760 | A3 | 19920707 | | |
| US 1992-40564 | A3 | 19930331 | | |
| US 1992-103961 | A1 | 19930809 | | |
| US 1994-306472 | A3 | 19940915 | | |
| US 1994-307273 | A3 | 19940916 | | |

AB: The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gtl1 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-96-8

AB: PRP,(Properties)
(nucleotide sequence of)

RN 155182-96-8 CAPLUS

DN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgcgt ggtcatagtg ggcagggtcg tcttgcgg gaagccggca
51 atcataacctg acagggaaatg cctctaccga gagttcgatg agatggaaaga

STN Columbus

101 gtgctctcag cacttaccgt acatcgagca agggatgatg ctcggccgagc
151 agttcaagca gaaggcccctc ggcctcctgc agaccgcgtc ccgtcaggca
201 gaggttatcg cccctgctgt ccagaccac tggaaaaac tggagacatt
251 ctggcgaag catatgtgaa acttcatacg tggataaca tacttggcgg
301 gcttgtcaac gtcgcctggt aaccccgcca ttgcttcatt gatggctttt
351 acagctgctg tcaccagccc actaaccact agccaaa

L18 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:32855 CAPLUS

DN 108:32855

TI Nucleotide sequence, promoter analysis, and linkage mapping of the unusually organized operon encoding ribosomal proteins S7 and S12 in maize chloroplast

AU Giese, Klaus; Subramanian, Alap R.; Larrinua, Ignacio M.; Bogorad, Lawrence

CS Abt. Wittmann, Max-Planck-Inst. Mol. Genet., Berlin, D-1000/33, Fed. Rep. Ger.

SO Journal of Biological Chemistry (1987), 262(31), 15251-5

====

CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB The nucleotide sequence of the operon encoding maize chloroplast ribosomal protein genes S7 and S12 and the promoter activity of a chimeric construct of the -10/-35 sequence of this operon (attached to a promoterless chloramphenicol acetyltransferase gene) were detd. This operon occurs in the chloroplast genome divided in 2 parts: part A contains exon 1 of rpS12 (encoding the N-terminal 38 amino acid residues), whereas part B has the following structure: promoter-rpS12 (exon 2 + intron + exon 3)-spacer-rps7-terminator. Part A is located at the approx. coordinate position 41,000, whereas 2 copies of part B are located at 2 distant locations in the genome at coordinate positions 18,700 and 120,200. This unusual organization of the S12 operon in maize (a monocot plant) is similar to that reported in a dicot and a lower plant. The deduced amino acid sequence of maize chloroplast S7 shows 43, 38, 71, and 85% and of S12 shows 66, 72, 91 and 90% sequence identity to the corresponding sequences of *Escherichia coli*, *Euglena gracilis*, *Marchantia polymorpha*, and *Nicotiana tabacum*, resp. The promoter upstream of rpS12 (part B) is transcriptionally active in *E. coli*.

IT 112263-07-7

RL: PAP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 112263-07-7 CAPLUS

CN DNA (corn chloroplast gene rps12 coding region) (9CI) (CA INDEX NAME)

NTE double stranded

SEQ 1 atgcctacta ttcaacaatt aattttttttt aaaaagacaac ccatcgaaaa
51 tagaagaaaa tcaccagccc ttaaaggatg ccctcaacgt agaggagat
101 gtactagatg gtatactatc aaccccaaaa aaccccaactc tgccttacgt
151 aaagtgtcca gagtacgatt aaccttctggaa ttgaaatca ctgcttataat
201 acctggattt ggcataatt tacaagaacaa ttctgttagta tttagtaagag
251 gaggaagggt taaggattttt cccgggtgtga gatatccat tatttcgagga
301 acccttagatg ctgtcgcaatg aaagaatcgta caacaaggc gttctaaata
351 tggggccaaa aagccaaaaa aataaa

STN Columbus

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| CA SUBSCRIBER PRICE | -1.46 | -5.11 |

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
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information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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STN Columbus

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FILE COVERS 1967 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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 L25 1 L24 AND PY<1990

=> d bib ab hitseq

L25 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
Full Text
 AN 1994296653 CAPLUS
 DN 120296653
 TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
 IN Houghton, Michael; Choo, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian. 157 pp.
 CODEN: INXXAP
 DT Patent
 LA English
 FAN:CNT 8
 PATENT NO. KIND DATE APPLICATION NO. DATE
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STN Columbus

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FL, RO, SD, SU | | | | |
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| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| | AT 139343 | E | 19960615 | AT 1991-302910 | 19910403 |
| | ES 2083465 | T3 | 19960816 | ES 1991-302910 | 19910403 |
| | AT 182684 | E | 19990815 | AT 1995-114016 | 19910403 |
| | ES 2134388 | T3 | 19991001 | ES 1995-114016 | 19910403 |
| | US 5683864 | A | 19971104 | US 1992-910760 | 19920707 |
| | FI 106317 | B1 | 20010115 | FI 1992-4349 | 19920928 |
| | NC 9203839 | A | 19921119 | NO 1992-3839 | 19921001 |
| | NO 310241 | B1 | 20010611 | | |
| | US 5714596 | A | 19980203 | US 1993-40564 | 19930331 |
| | LV 10336 | B | 19950620 | LV 1993-442 | 19930531 |
| | LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
| | US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |

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| US 5350671 | A | 19940927 | US 1993-103961 | 19930809 |
| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
| HR 940493 | B1 | 20001031 | HR 1994-940493 | 19940907 |
| US 5698390 | A | 19971216 | US 1994-306472 | 19940915 |
| US 6074816 | A | 20000613 | US 1994-307273 | 19940916 |
| US 5712087 | A | 19980127 | US 1995-440519 | 19950512 |
| US 6312889 | B1 | 20011106 | US 1995-440549 | 19950512 |
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| US 6096541 | A | 20000801 | US 1995-441026 | 19950515 |
| US 6171782 | B1 | 20010109 | US 1995-442647 | 19950515 |
| US 6861212 | B1 | 20050301 | US 1995-441355 | 19950515 |
| US 5863719 | A | 19990126 | US 1995-472821 | 19950607 |
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| NO 306511 | B1 | 19991115 | | |
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| NO 303879 | B1 | 19980914 | | |
| US 2003162167 | A1 | 20030828 | US 1996-686983 | 19960725 |
| JP 09173079 | A2 | 19970708 | JP 1996-241451 | 19960822 |
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| FI 9801380 | A | 19980615 | FI 1998-1380 | 19980615 |
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| GR 3031361 | T3 | 20000131 | GR 1999-402455 | 19990929 |
| PRAI US 1987-122714 | A | 19871118 | | |
| IN 1988-CA960 | A | 19881118 | | |
| US 1987-139886 | A | 19871230 | | |
| US 1988-161072 | A | 19880226 | | |
| US 1983-191263 | A | 19880506 | | |
| US 1988-263584 | A | 19881026 | | |
| US 1988-271450 | A | 19881114 | | |
| CN 1988-107988 | A | 19881118 | | |
| JP 1992-361785 | A3 | 19881118 | | |
| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
| JP 1996-241451 | A3 | 19881118 | | |
| JP 1998-2111631 | A3 | 19881118 | | |
| WO 1998-US4125 | A | 19881118 | | |
| YU 1998-2138 | A6 | 19881118 | | |
| US 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353896 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
| US 1989-355961 | B2 | 19890518 | | |
| NO 1989-2931 | A | 19890717 | | |
| US 1989-398667 | B2 | 19890825 | | |
| US 1989-456637 | B2 | 19891221 | | |
| US 1990-504352 | A | 19900404 | | |
| US 1990-505435 | B2 | 19900404 | | |
| US 1990-566209 | B1 | 19900808 | | |
| US 1990-611965 | B2 | 19901108 | | |
| WO 1991-US2225 | A | 19910329 | | |
| EP 1991-302910 | A3 | 19910403 | | |
| US 1992-910760 | A3 | 19920707 | | |
| US 1993-40564 | A3 | 19930331 | | |
| US 1993-103961 | A1 | 19930809 | | |
| US 1994-306472 | A3 | 19940915 | | |
| US 1994-307273 | A3 | 19940916 | | |

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA

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suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctgcgt ggtcatagtg ygcagggtcg tcttgcggcga
51 atcataacctg acagggaaatg cctctaccga gagttcgatg agatggaaga
101 gtgctctcag cacttaccgt acatcgagca agggatgtatc ctcggccgac
151 agttcaagca gaaggccctc ggcctctgc agaccgcgtc ccgtcaggca
201 gaggttatcg cccctgctgt ccagaccaa tggcaaaaac tcgagacatt
251 ctggggcgaag catatgtgga acttcatcag tgggatacaa tacttggcgg
301 gcttgcacac gctgcctggta aaccccgcca ttgcttcatt gatggctttt
351 acagctgctg tcaccagccc actaaccact agccaaa

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| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | -0.73 | -5.84 |

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* available and contains the CA role and document type information. *

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

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STN Columbus

=> d bib ab hitseq 1-3

L30 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV
(hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian, 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN.CNT 8

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| PI | IN 171237 | A | 19920822 | IN 1990-CA801 | 19900917 |
| | AU 8927967 | A1 | 19890614 | AU 1989-27967 | 19881118 <-- |
| | AU 624105 | B2 | 19920604 | | |
| | ZA 8808669 | A | 19890830 | ZA 1988-8669 | 19881118 <-- |
| | BR 8807310 | A | 19900313 | BR 1988-7310 | 19881118 |
| | DD 287104 | A5 | 19910214 | DD 1988-321971 | 19881118 |
| | IN 169067 | A | 19910831 | IN 1988-CA960 | 19881118 |
| | DD 298524 | A5 | 19920227 | DD 1988-344401 | 19881118 |
| | DD 298525 | A5 | 19920227 | DD 1988-344402 | 19881118 |
| | DD 298526 | A5 | 19920227 | DD 1988-344403 | 19881118 |
| | DD 298527 | A5 | 19920227 | DD 1988-344404 | 19881118 |
| | CN 1073719 | A | 19930630 | CN 1992-110257 | 19881118 |
| | CN 1073722 | B | 20011107 | | |
| | JP 090801600 | B4 | 19931115 | JP 1989-500565 | 19881118 |
| | JP 09101844 | A2 | 19970715 | JP 1996-239921 | 19881118 |
| | JP 10008674 | A2 | 19980428 | JP 1997-99651 | 19881118 |
| | JP 10230696 | A2 | 19981104 | JP 1998-111631 | 19881118 |
| | JP 10230697 | A2 | 19981104 | JP 1998-111632 | 19881118 |
| | JP 2000023683 | A2 | 20000125 | JP 1999-157193 | 19881118 |
| | RU 21364394 | C2 | 20010210 | RU 1988-4742221 | 19881118 |
| | FI 3903447 | A | 19890717 | FI 1989-3447 | 19890717 <-- |
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| | NO 8902931 | A | 19890913 | NO 1989-2931 | 19890717 <-- |
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| | DK 9903537 | A | 19890718 | DK 1989-3537 | 19890718 <-- |
| | KR 136776 | B1 | 19980515 | KR 1989-701343 | 19890718 |
| | IN 171238 | A | 19920822 | IN 1990-CA802 | 19900917 |
| | IN 171239 | A | 19920822 | IN 1990-CA805 | 19900917 |
| | IN 171240 | A | 19920822 | IN 1990-CA808 | 19900917 |
| | WO 9115771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
| | W: AU, BB, BG, BR, CA, FI, GB, HU, JP, KP, KR, LK, MC, MG, MW, NO, | | | | |
| | PL, RO, SD, SU | | | | |
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| | AU 9176510 | A1 | 19911030 | AU 1991-76510 | 19910329 |
| | AU 639560 | B2 | 19930729 | | |
| | GB 2257784 | A1 | 19930120 | GB 1992-20480 | 19910329 |
| | BR 9106309 | A | 19930420 | BR 1991-6309 | 19910329 |
| | HU 62706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| | HU 217025 | B | 19991129 | | |
| | JP 05508219 | T2 | 19931118 | JP 1991-507636 | 19910329 |
| | JP 2733138 | B2 | 19980330 | | |
| | RO 109916 | B1 | 19950728 | RO 1975-92012 | 19910329 |
| | PL 172133 | B1 | 19970829 | PL 1991-296329 | 19910329 |
| | RU 2130969 | C1 | 19990527 | RU 1991-5053084 | 19910329 |
| | EP 450931 | A1 | 19911009 | EP 1991-302910 | 19910403 |

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| EP 450931 | B1 | 19960612 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| EP 693G87 | A1 | 19960124 | EP 1995-114016 | 19910403 |
| EP 693687 | B1 | 19990728 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
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| ES 2088465 | T3 | 19960816 | ES 1991-302910 | 19910403 |
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| ES 2134388 | T3 | 19991001 | ES 1995-114016 | 19910403 |
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| NO 310241 | B1 | 20010611 | | |
| US 5714596 | A | 19980203 | US 1993-40564 | 19930331 |
| LV 10306 | B | 19950620 | LV 1993-442 | 19930531 |
| LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
| US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |
| US 5350671 | A | 19940927 | US 1993-103961 | 19930809 |
| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
| HR 940493 | B1 | 20001031 | HR 1994-940493 | 19940907 |
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| JP 1992-1793 | B2 | 20010604 | | |
| FI 1998-1380 | A | 19980615 | FI 1998-1380 | 19980615 |
| PT 1995-5641 | B1 | 20010228 | | |
| GR 3001361 | T3 | 20000131 | GR 1999-402455 | 19990929 |
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| CM 1988-107988 | A | 19881118 | | |
| JP 1992-361785 | A3 | 19881118 | | |
| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
| JP 1996-241451 | A3 | 19881118 | | |
| JP 1998-111631 | A3 | 19881118 | | |
| WO 1988-US4125 | A | 19881118 | | |
| YU 1988-2138 | A6 | 19881118 | | |
| UF 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353896 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
| US 1989-355961 | B2 | 19890518 | | |
| NO 1989-2931 | A | 19890717 | | |
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| US 1990-504352 | A | 19900404 |
| US 1990-505435 | B2 | 19900404 |
| US 1990-566209 | B1 | 19900808 |
| US 1990-611965 | B2 | 19901108 |
| WO 1991-US2225 | A | 19910329 |
| EP 1991-302910 | A3 | 19910403 |
| US 1992-910760 | A3 | 19920707 |
| US 1993-40564 | A3 | 19930331 |
| US 1993-103961 | A1 | 19930809 |
| US 1994-306472 | A3 | 19940915 |
| US 1994-307273 | A3 | 19940916 |

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunocassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-96-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-96-8 CAPLUS

CN DNA (Hepatitis C virus polyprotein 128-amino acid fragment--specifying)
(94%) (CA INDEX NAME)

SEQ 1: cggactgcgt agtcatactg ggcagggtcg tcttgccgg gaagccggca
51: acataccctg acagggaaat ccttacccga gagttcgtat agatggaaaga
101: gtgtctccat cacttaccgt acatcgacca agggatgtat ctcggccgac
151: gttcaagca gaaggccctc ggcctctgc agaccgcgtc ccgtcaggca
201: gaggttatacg cccctgtgtt ccagaccac tggaaaaac tcgagacatt
251: ctggggcgaag catatgttggaa acttcatcgat tggatataaa tacttggcgg
301: gttgtcaac gtcgttgtt aaccccgcca ttgcttcatt gatggcttt
351: acagctgtgtc tcaccagccc actaaccact agccaaa

L30 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:547329 CAPLUS

DN 105:147329

TI A genetically engineered murine/human chimeric antibody retains specificity for human tumor-associated antigen

AU Sahagian, Barbara G.; Dorai, Haimanti; Saltzgaber-Muller, Jo; Toneguzzo, Francisco; Guindon, Cathy A.; Lilly, Sarah P.; McDonald, Kevin W.; Morrissey, David V.; Stone, Barry A.; et al.

CS New Technol. Res., E. I. DuPont de Nemours and Co., Billerica, MA, 01862; USA

SO Journal of Immunology (1986), 137(3), 1066-74

====

CODEN: JOIMAS; ISSN: 0022-1767

DT Journal

LA English

OS CASREACT 105:147329

AB Chimeric immunoglobulin genes were constructed by fusing murine variable

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region exons to human const. region exons. The ultimate goal was to produce an antibody capable of escaping surveillance by the human immune system while retaining the tumor specificity of a murine monoclonal. The murine variable regions were isolated from the functionally expressed κ and γ 1 immunoglobulin genes of the murine hybridoma cell line B6.2, the secreted monoclonal antibody of which reacts with a surface antigen from human breast, lung, and colon carcinomas. The κ and γ 1 chain fusion genes were cointroduced into non-antibody-producing murine myeloma cells by electroporation. Transfectants that produced murine/human chimeric antibody were obtained at high frequency, as indicated by immunoblots probed with an antisera specific for human Ig. Enzyme-linked immunoabsorbent assay anal. demonstrated that this chimeric antibody was secreted from the myeloma cells and retained the ability to bind selectively to membrane prep'd. from human tumor cells. The chimeric Ig was also shown by indirect fluorescence microscopy to bind to intact human carcinoma cells with the specificity expected of B6.2. The ability of chimeric antibody to recognize human tumor-assocd. antigen makes feasible a novel approach to cancer immunotherapy.

IT 104491-32-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 104491-32-9 CAPLUS

CN DNA (mouse clone pSV2gpt/B6.2VLHuCK B6.2 immunoglobulin G 1
κ-chain fragment-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 gacattgtga tgacccagtc tcaaaaattc atgtccacat cagtggaga
51 cagggtcagc gtcacctgca aggccagtc gaatgtggtc actaatgttag
101 ttcttgtatca acagacaccaggacaatctc ctaaaagact gatttactcg
151 gatccctacc ggtacagttgg agtccctgtat cgcttctcag gcaatggacc
201 tggacatcat ttcactctca ccatcagcaa tgtgcagtct ggagacttgg
251 ccaggatattt tcgtcagcaa tataaagct atccctctcac gttcggtgct
301 gggaccaage tggactgaa acgg

L30 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS ON STN

Full Text

AN 1985:18693 CAPLUS

DN 102:18693

TI Characterization of three chicken pseudogenes for U1 RNA

AU Kristo, Paula; Tsai, Ming Jer; O'Malley, Bert W.

CS Dep. Cell Biol., Baylor Coll. Med., Houston, TX, 77030, USA

SO DNA (1984), 3(4), 281-6

CODEN: DNAADR; ISSN: 0193-0238

DT Journal

LA English

AB Three chicken genomic DNA clones contg. the U1 RNA sequence were isolated from a chicken gene library and characterized. Two of these clones, CL64 and CL41, are overlapping clones which show several single-nucleotide changes in the U1 coding sequence, suggesting that they probably are alleles of the same sequence. The U1 sequence in the 3rd clone, CL40, is more divergent. Flanking regions of these genes do not share any sequence homol. between each other or with the previously isolated chicken genomic clone CL59. A short repeat CGGGG appears 28 times upstream of the U1 sequence in CL59. Another repeat, GCACC, is repeated 14 times upstream of the U1 region in CL40.

IT 93927-63-0

RL: PRP (Properties)

STN Columbus

(characterization and sequence for)
PN 93927-63-0 CAPLUS
CN DNA (chicken clone CL40 U1 RNA pseudogene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 ttaccttgac ccgcctgagg ttttccatt gctctggca ggaggatgtt
51 acccagatgt gggtagcgct gaaatccatc ctttcagccg tgattcagtg
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151 gctctgtggg

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| CA SUBSCRIBER PRICE | -2.19 | -8.03 |

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DICTIONARY FILE UPDATES: 23 APR 2005 HIGHEST RN 849459-72-9

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TECA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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STN Columbus

(TGCTGTCCAG/SQEN AND SQL=10)

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L33 6562 L32 AND SQL<400

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| CA SUBSCRIBER PRICE | 0.00 | -8.03 |

FILE 'CPLUS' ENTERED AT 16:00:16 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP.USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s l33
L34 6562 L33

=> s l34 and PY<1990
13006711 PY<1990
L35 3 L34 AND PY<1990

=> d bib ab hitseq

L35 ANSWER 1 OF 1 CPLUS COPYRIGHT 2005 ACS on STN
Full Text.
AN 1994:296653 CPLUS
DN 120:296653
TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
IN Houghton, Michael; Choo, Qui Lim; Kuo, George
PA Chiron Corp., India
SO Indian, 157 pp.
CODEN: INXXAP
DT Patent

STN Columbus

LA English

FAN CNT 8

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| PI | IN 171237 | A | 19920822 | IN 1990-CA801 | 19900917 |
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| | AU 624105 | B2 | 19920604 | | |
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| | BR 8207310 | A | 19900313 | BR 1988-7310 | 19881118 |
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| | IN 169067 | A | 19910831 | IN 1988-CA960 | 19881118 |
| | DD 298524 | A5 | 19920227 | DD 1988-344401 | 19881118 |
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| | CN 1073719 | A | 19930630 | CN 1992-110257 | 19881118 |
| | CN 1074422 | B | 20011107 | | |
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| | IN 199209 | A | 19920822 | IN 1990-CA805 | 19900917 |
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| | WO 9105771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
| | W: AU, BB, BG, BR, CA, FI, GB, HU, JP, KP, KR, LK, MC, MG, MW, NC,
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| | AU 919360 | B2 | 19930729 | | |
| | GB 2257784 | A1 | 19930120 | GB 1992-20480 | 19910329 |
| | BR 9106309 | A | 19930420 | BR 1991-6309 | 19910329 |
| | HU 62706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| | HU 227025 | B | 19991129 | | |
| | JP 09508219 | T2 | 19931118 | JP 1991-507636 | 19910329 |
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| | RO 109916 | B1 | 19950728 | RO 1975-92012 | 19910329 |
| | PL 172133 | B1 | 19970329 | PL 1991-296329 | 19910329 |
| | RU 2130969 | C1 | 19990527 | RU 1991-5053084 | 19910329 |
| | EP 450931 | A1 | 19911009 | EP 1991-302910 | 19910403 |
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STN Columbus

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| LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
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| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
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| WO 1988-US4125 | A | 19881118 | | |
| YU 1988-2138 | A6 | 19881118 | | |
| US 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353896 | B2 | 19890421 | | |
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| US 1989-355961 | B2 | 19890518 | | |
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| US 1989-456637 | B2 | 19891221 | | |
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| US 1990-611965 | B2 | 19901108 | | |
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| US 1993-40564 | A3 | 19930331 | | |
| US 1993-103961 | A1 | 19930809 | | |
| US 1994-306472 | A3 | 19940915 | | |
| US 1994-307273 | A3 | 19940916 | | |

A3 The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also

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provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

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=> file registry

COST IN U.S. DOLLARS

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FULL ESTIMATED COST

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*
* The CA roles and document type information have been removed from *

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* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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STN Columbus

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L40 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
 DN 120:296653
 TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
 IN Houghton, Michael; Choo, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian, 157 pp.
 CODEN: INXXAP
 DT Patent
 LA English
 FAN.CNT 8

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STN Columbus

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| EP 693687 | B1 | 19990728 | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | |
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| LV 10306 | B | 19950620 | LV 1993-4381 | 19930531 |
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STN Columbus

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| WO 1991-US2225 | A | 19910329 |
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| US 1993-103961 | A1 | 19930809 |
| US 1994-306472 | A3 | 19940915 |
| US 1994-307273 | A3 | 19940916 |

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-84-6, DNA (hepatitis C virus clone 5-1-1 cDNA)

155182-86-8 155182-87-9, DNA (hepatitis C virus clone

cDNA)

SL: PEP (Properties)

(nucleotide sequence of)

RN 155182-84-6 CAPLUS

CN DNA (hepatitis C virus clone 5-1-1 polyprotein fragment-specifying) (9CI) (CA INDEX NAME)

SEQ :1 ggcctcctgc ttgaactgct cggcgagcat catacctgac agggaaagtcc
51 tctaccgaga gttcgatgag atggaaaggt gctctcagca cttaccgtac
101 atcgagcaag ggatgatgct cggccggcgg ttcaaggcaga aggccctcggt
151 cctcc

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying) (9CI) (CA INDEX NAME)

SEQ :1 ctggctgcgt ggtcatgtg ggcagggtcg tcttgccgg gaagccggca
51 atcataacctg acaggaaatgt tctaccga gagttcgatg agatggaaaga
101 gtgctctcg cacttaccgt acatcgagca agggatgatg ctcgcggc
151 agttcaagca gaaggccctc ggcctcgtgc agaccggcgtc cggcggc
201 gaggttatcg cccctgtgt ccagaccaa tggcaaaaac tcgagacctt
251 ctggggcaag catatgttgc acttcatcg tggatataaa tacttggcgg
301 gcttgtcaac gctgcgttgt aacccggcca ttgcttcatt gatggctttt
351 acagctgcty tcaccayccc actaaccact agccaaa

RN 155182-87-9 CAPLUS

STN Columbus

CN DNA (hepatitis C virus clone 1-2 164-nucleotide fragment) (9CI) (CA INDEX NAME)

SEQ 1 ggtcatagtg ggcagggtcg tcttgcgg gaagccggca atcataacctg
 51 acagggaaagt cctctatcga gagttcgatg agatgaaaga gtgtctcag
 101 cacttaccgt acatcgagca agggatgtatg ctgcggcagc agttcaagca
 151 gaaggccctc ggcc

L40 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:230854 CAPLUS

DN 112:230854

TI Synthetic gene encoding human interleukin 5

IN Edwards, Richard Mark

PA British Bio-Technology Ltd., UK

SO Brit. UK Pat. Appl., 21 pp.

CODEN: BAXXDU

DT Patent

LA English

FAN.CNT 1

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|------|----------|-----------------|--------------|
| PI GB 2217328 | A1 | 19891025 | GB 1988-8524 | 19880412 <-- |
| GB 2217328 | B2 | 19920129 | | |

PI/AI GB 1988-8524 19880412

AB A synthetic gene encoding human interleukin-5 is described. The gene contains restriction sites at frequent intervals to facilitate cassette mutagenesis. The gene also is flanked by restriction sites which simplifies its incorporation into desired expression systems. The gene was cloned in Escherichia coli.

IV 127314-99-2

RD: PROPERTIES (Properties)

(nucleotide sequence of and cloning in Escherichia coli of)

RF 127314-99-2 CAPLUS

CN DNA (human clone ph.IL-5-30 interleukin 5 [Met-1]-specifying plus flanks) (9CI) (CA INDEX NAME)

SEQ 1 aacgttaccc gccatggaaa ttcccactag tgcatggtg aaagagaccc
 51 tggcactgct ttctactcat cgaactctgc tgatagccaa ttagactctc
 101 cggattcccg ttctgtaca taaaaatcac caactgtgca ctgaagaaat
 151 ctttcaggaa ataggcacac tcgagagtcu uactgtgcaa gggggtaact
 201 tggaaagact attcaaaaac ttgtccttaa taaagaaaata catcgatggc
 251 caaaaaaaaaa agtgtggaga agaaagacgg agatgtaaacc aattccatgg
 301 ctatctgcag gagtttcttg gtgtatgaa caccgagtgg ataatagaaa
 351 gttgataagg atccgaattc

>> file registry
 COST IN U.S. DOLLARS

TOTAL ESTIMATED COST

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| 18.24 | 421.55 |

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

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to the file summary sheet on the web at:
<http://www.acs.org/CNLIN/DBSS/registryss.html>

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L41 0 GGCTCCTGC/SQEN
(GGCTCCTGC/SQEN AND SQL=10)

=> s ggctcgc/sqsn and SQL<400
SYSTEM LIMIT EXCEEDED -- SEARCH ENDED
The search profile you entered was too complex or gave too many
answers. Simplify or subdivide the query and try again. If you have
exceeded the answer limit, enter DELETE HISTORY at an arrow prompt
(=>) to remove all previous answers sets and begin at L1. Use the
SAVE command to store any important profiles or answer sets before
using DELETE HISTORY.

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| 40.24 | 461.79 |

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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=> A L4 AND PY<1990
 AC038V11 PY<1990
 L45 A L44 AND PY<1990

=> d b1b ab hitseq 1 2

L45 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 19940206653 CAPLUS
 DN 32012906653
 TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
 IN Hoaglin, Michael; Chico, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian, 157 pp.
 CC'DENY ENXXAP
 DT Patent
 LA English

FAN.CNT 8

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| AU 624105 | B2 | 19920604 | | |
| ZA 3803669 | A | 19890830 | ZA 1988-8669 | 19881118 <-- |
| BR 3807310 | A | 19900313 | BR 1988-7310 | 19881118 |
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STN Columbus

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| DD 298527 | A5 | 19920227 | DD 1988-344404 | 19881118 |
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| JP 05081600 | B4 | 19931115 | JP 1989-500565 | 19881118 |
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| JP 10290697 | A2 | 19981104 | JP 1998-111632 | 19881118 |
| JP 2000023683 | A2 | 20000125 | JP 1999-157193 | 19881118 |
| RU 2162894 | C2 | 20010210 | RU 1988-4742221 | 19881118 |
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| NO 8902931 | A | 19890913 | NO 1989-2931 | 19890717 <-- |
| NO 304990 | B1 | 19990315 | | |
| DK 8903537 | A | 19890718 | DK 1989-3537 | 19890718 <-- |
| KR 138776 | B1 | 19980515 | KR 1989-701343 | 19890718 |
| IN 171238 | A | 19920822 | IN 1990-CA802 | 19900917 |
| IN 171239 | A | 19920822 | IN 1990-CA805 | 19900917 |
| IN 171240 | A | 19920822 | IN 1990-CA808 | 19900917 |
| WO 9115771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
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PL, RO, SD, SU | | | | |
| RW: BF, BJ, CF, CG, CM, GA, ML, MR, SN, TD, TG | | | | |
| AU 9176510 | A1 | 19911030 | AU 1991-76510 | 19910329 |
| AU 639560 | B2 | 19930729 | | |
| GB 2257784 | A1 | 19930120 | GB 1992-20480 | 19910329 |
| BR 9106309 | A | 19930420 | BR 1991-6309 | 19910329 |
| HU 62706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| EP 117025 | B | 19991129 | | |
| JP 05568219 | T2 | 19931118 | JP 1991-507636 | 19910329 |
| JP 2783138 | B2 | 19980330 | | |
| RO 100916 | B1 | 19950728 | RO 1975-92012 | 19910329 |
| PL 172133 | B1 | 19970829 | PL 1991-296329 | 19910329 |
| RU 2130969 | C1 | 19990527 | RU 1991-5053084 | 19910329 |
| EP 450931 | A1 | 19911009 | EP 1991-302910 | 19910403 |
| EP 450931 | B1 | 19960612 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| EP 693687 | A1 | 19960124 | EP 1995-114016 | 19910403 |
| EP 693687 | B1 | 19990728 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| AT 139343 | E | 19960615 | AT 1991-302910 | 19910403 |
| ES 2086465 | T3 | 19960816 | ES 1991-302910 | 19910403 |
| AT 132684 | S | 19990815 | AT 1995-114016 | 19910403 |
| ES 3134388 | T3 | 19991001 | ES 1995-114016 | 19910403 |
| US 5693864 | A | 19971104 | US 1992-910760 | 19920707 |
| FI 106617 | B1 | 20010115 | FI 1992-4349 | 19920928 |
| NO 9203839 | A | 19921119 | NO 1992-3839 | 19921001 |
| NO 310241 | B1 | 20010611 | | |
| US 5714596 | A | 19930203 | US 1993-40564 | 19930331 |
| LV 10306 | B | 19950620 | LV 1993-442 | 19930531 |
| LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
| US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |
| US 5350671 | A | 19940927 | US 1993-103961 | 19930809 |
| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
| HR 940493 | B1 | 20001031 | HR 1994-940493 | 19940907 |
| US 5698390 | A | 19971216 | US 1994-306472 | 19940915 |
| US 6074816 | A | 20000613 | US 1994-307273 | 19940916 |
| US 5712087 | A | 19980127 | US 1995-440519 | 19950512 |
| US 5312889 | B1 | 20011106 | US 1995-440549 | 19950512 |
| US 5712088 | A | 19980127 | US 1995-440769 | 19950515 |
| US 5096541 | A | 20000801 | US 1995-441026 | 19950515 |

STN Columbus

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| US 6171782 | B1 | 20010109 | US 1995-442647 | 19950515 |
| US 6861212 | B1 | 20050301 | US 1995-441355 | 19950515 |
| US 5863719 | A | 19990126 | US 1995-472821 | 19950607 |
| NO 9505101 | A | 19951215 | NO 1995-5101 | 19951215 |
| NO 306511 | B1 | 19991115 | | |
| NO 9505102 | A | 19951215 | NO 1995-5102 | 19951215 |
| NO 303879 | B1 | 19980914 | | |
| US 2003162167 | A1 | 20030828 | US 1996-686983 | 19960725 |
| JP 09173079 | A2 | 19970708 | JP 1996-241451 | 19960822 |
| JP 3171793 | B2 | 20010604 | | |
| FI 9801380 | A | 19980615 | FI 1998-1380 | 19980615 |
| FI 106564 | B1 | 20010228 | | |
| GR 3031361 | T3 | 20000131 | GR 1999-402455 | 19990929 |
| PRAI US 1987-122714 | A | 19871118 | | |
| IN 1989-CA960 | A | 19881118 | | |
| US 1987-139886 | A | 19871230 | | |
| US 1988-161072 | A | 19880226 | | |
| US 1988-191263 | A | 19880506 | | |
| US 1988-263584 | A | 19881026 | | |
| US 1988-271450 | A | 19881114 | | |
| CN 1988-107988 | A | 19881118 | | |
| JP 1992-361785 | A3 | 19881118 | | |
| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
| JP 1996-241451 | A3 | 19881118 | | |
| JP 1998-111631 | A3 | 19881118 | | |
| WO 1988-US4125 | A | 19881118 | | |
| WU 1988-2138 | A6 | 19881118 | | |
| US 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-253896 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
| US 1989-355961 | B2 | 19890518 | | |
| US 1989-2931 | A | 19890717 | | |
| US 1990-398667 | B2 | 19890825 | | |
| US 1990-456637 | B2 | 19901221 | | |
| US 1990-504352 | A | 19900404 | | |
| US 1990-505435 | B2 | 19900404 | | |
| US 1990-566209 | B1 | 19900808 | | |
| US 1990-611965 | B2 | 19901108 | | |
| WO 1990-US2225 | A | 19910329 | | |
| EP 1991-302910 | A3 | 19910403 | | |
| US 1991-910760 | A3 | 19920707 | | |
| US 1993-40564 | A3 | 19930331 | | |
| US 1993-103961 | A1 | 19930809 | | |
| US 1994-306472 | A3 | 19940915 | | |
| US 1994-307273 | A3 | 19940916 | | |

AB The single kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-84-5, DNA (hepatitis C virus clone 5-1-1 cDNA)
155182-86-8

STN Columbus

RL: PRP (Properties)
(nucleotide sequence of)
RN 155182-84-6 CAPLUS
CN DNA (hepatitis C virus clone 5-1-1 polyprotein fragment-specifying) (9CI)
(CA INDEX NAME)

SEQ 1 ggccctcgtc ttgaactgct cggcgagcat cataacctgac agggaaagtcc
51 tctaccgaga gttcgatgag atggaagagt gctctcagca cttaccgtac
101 atcgagcaag ggatgatgct cgccgagcag ttcaagcaga aggccctcg
151 cctcc

RN 155182-86-8 CAPLUS
CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

SEQ 1 ctggctcggt ggtcatagtg ggcagggtcg tcttgcggga gaagccggca
51 atcataacctg acagggaaat cctctaccga gagttcgatg agatgaaaga
101 gtgctctcgacttaccgt acatcgagca agggatgatg ctcggcggc
151 agttcaagca gaagggccctc ggccctctgc agaccgcgtc ccgtcaggca
201 gaggttatacg cccctgtgtt ccagaccaac tggcaaaaac tcgagacatt
251 ctgggcgaag catatgttga acttcatcgat tgggatataa tacttggcg
301 gcttgtcaac gctgcctggta aacccgccta ttgcttcatt gatggtttt
351 acayctgtgt tcaccagccc actaasact agccaaa

L43 0.0918 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

BN 155186-22 CAPLUS
CW 155186-22
TI Genes for tRNA and their putative expression signals in Methanococcus
AU Reich, Guenter; Sibold, Lionel; Boeck, August
CS Univ. Muenchen, Munich, 8000/19, Fed. Rep. Ger.
SO Systematic and Applied Microbiology (1986), 7(1), 18-25
====

CODEN: SAMIDF; ISSN: 0723-2020

DT Journal

LA English

AB A no. of tRNA genes from *M. vannielii* were cloned and sequenced. They belong to 6 putative transcriptional units comprising 11 tRNA genes. Together with the tRNA gene sequences previously reported, this brings the total of *Methanococcus* tRNA genes now analyzed to 19, organized in 7 putative transcriptional units. In 2 of the tRNA gene clusters (one comprising 2 genes, the other, 6 genes) one of the genes possesses opposite transcriptional polarity and is sep'd. from the remaining gene(s) by a spacer of 146 and 115 nucleotides, resp. Comparison of the region flanking the 7 transcriptional units at the 5' end yielded a consensus sequence between -25 and -50 bases upstream. In the tRNA gene clusters with opposite transcriptional polarity this sequence occurred twice and also in inverse polarity. This observation and the fact that this sequence was the only detectable motif of homologous primary structures in 5'-upstream regions of tRNA genes indicates that it may be involved in transcription initiation. Common motifs at the 3'-flanking regions, which may possibly be involved in transcription termination, are also presented.

IT 104245-31-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

STN Columbus

RN 104245-31-0 CAPLUS
CN DNA (Methanococcus vannielii tRNATHr GGU gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 agccttaggc ggggttgaa cccgcggctt cctgcttacc aagcaggcgc
51 tctaccaggc tgagccactg agyc

| | | |
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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:

<http://www.cas.org/ONLINE/DBSS/registryss.html>

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STN Columbus

L47 13729 AGACCGCGTC/SQSN

=> s 147 and SQL<400
 22713436 SQL<400
 L48 1216 L47 AND SQL<400

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FILE CAPLUS - 29 Apr 2005 VOL 142 ISS 19
 FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 146
 L49 E78,L48
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 L50 a L49 AND PY<1990
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L50 ~~13729~~ 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
Full Text
 AN 20061296653 CAPLUS
 DN 120696653
 TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis-C virus) in biological samples such as blood serum
 IN McGuigan, Michael; Choo, Qui Lim; Kuò, George
 PA Chiron Corp., India
 SO India 157 pp.
 C00001111XXA#
 DT Patent
 LN English
 FAN:ENT 3
 PATENT NO. KIND DATE APPLICATION NO. DATE

STN Columbus

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| | AU 624105 | B2 | 19920604 | | |
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| | JP 10290697 | A2 | 19981104 | JP 1998-111632 | 19881118 |
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| | KR 138776 | B1 | 19980515 | KR 1989-701343 | 19890718 |
| | IN 171238 | A | 19920822 | IN 1990-CA802 | 19900917 |
| | IN 171239 | A | 19920822 | IN 1990-CA805 | 19900917 |
| | IN 171240 | A | 19920822 | IN 1990-CA808 | 19900917 |
| | WO 9115771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
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| | AT 91176510 | A1 | 19911030 | AU 1991-76510 | 19910329 |
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| | GB 2057784 | A1 | 19930120 | GB 1992-20480 | 19910329 |
| | BR 9106309 | A | 19930420 | BR 1991-6309 | 19910329 |
| | HU 62706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| | HU 217025 | B | 19991129 | | |
| | JP 05508219 | T2 | 19931118 | JP 1991-507636 | 19910329 |
| | JP 2733138 | B2 | 19980330 | | |
| | RO 1969916 | B1 | 19950728 | RO 1975-92012 | 19910329 |
| | PL 171133 | B1 | 19970829 | PL 1991-296329 | 19910329 |
| | RU 2110969 | C1 | 19990527 | RU 1991-5053084 | 19910329 |
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| | US 5683864 | A | 19971104 | US 1992-910760 | 19920707 |
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| | LV 10306 | B | 19950620 | LV 1993-442 | 19930531 |
| | LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |

STN Columbus

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| US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |
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| US 2003162167 | A1 | 20030828 | US 1996-686983 | 19960725 |
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| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
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| JP 1998-511631 | A3 | 19881118 | | |
| WO 1988-US4125 | A | 19881118 | | |
| YU 1988-2138 | A6 | 19881118 | | |
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| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353896 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
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| US 1993-103961 | A1 | 19930809 | | |
| US 1994-306472 | A3 | 19940915 | | |
| US 1994-307273 | A3 | 19940916 | | |

(E) The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV

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epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-86-8

RL: PRP (Properties)
(nucleotide sequence of)

RN 155182-86-8 CAPLUS

CN DNA (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(9CI) (CA INDEX NAME)

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** FILE REGISTRY
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FULL ESTIMATED COST

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DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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TMCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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* The CA roles and document type information have been removed from *
* the IDS default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *

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*

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

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FILE "CAPLUS" ENTERED AT 16:13:55 ON 29 APR 2005
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FILE: CAPLUS 1907 - 29 Apr, 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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STN Columbus

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LSS ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS
 DN 120:296653
 TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum
 IN Houghton, Michael; Choo, Qui Lim; Kuo, George
 PA Chiron Corp., India
 SO Indian, 157 pp.
 CODEN: INXXAP
 DT Patent
 LA English

FAN.CNT 8

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| | BR 8807310 | A | 19900313 | BR 1988-7310 | 19881118 |
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| | IN 169067 | A | 19910831 | IN 1988-CA960 | 19881118 |
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| | DD 298526 | A5 | 19920227 | DD 1988-344403 | 19881118 |
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| | CN 1073719 | A | 19930630 | CN 1992-110257 | 19881118 |
| | JP 1074422 | B | 20011107 | | |
| | JP 05001600 | A4 | 19931115 | JP 1989-500565 | 19881118 |
| | EP 05504844 | A2 | 19970715 | EP 1996-239921 | 19881118 |
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| | JP 10210696 | A2 | 19981104 | JP 1998-111631 | 19881118 |
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| | JP 2000023683 | A2 | 20000125 | JP 1999-157193 | 19881118 |
| | RU 2142894 | C2 | 20010210 | RU 1988-4742221 | 19881118 |
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REGISTRY INITIATED

Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L57 0 L56

=> file registry

CCST IN U.S. DOLLARS

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

CA SUBSCRIBER PRICE

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
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*

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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L61 ANSWER 1 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN
Full TEXT
AN 1994:597650 CAPLUS
DB 121:197650
TI Method for HLA DP typing
IN Erlich, Henry A.; Horn, Glenn T.; Bugawan, Teodorica; Begovich, Ann B.

STN Columbus

PA Hoffmann-La Roche, Inc., USA
 SO U.S., 22 pp. Cont.--in-part of U.S. Ser. No. 258,212, abandoned.
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DT Patent

LA English

FAN.CNT 27

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
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| | CA 1339206 | A1 | 19970805 | CA 1989-600226 | 19890519 |
| | US 5541065 | A | 19960730 | US 1994-195615 | 19940214 |
| | JP 10155500 | A2 | 19980616 | JP 1997-281834 | 19971015 |
| | JP 3070837 | B2 | 20000731 | | |
| | JP 2000189198 | A2 | 20000711 | JP 2000-52306 | 20000224 |
| | JP 3124528 | B2 | 20010115 | | |
| | JP 2000189199 | A2 | 20000711 | JP 2000-52307 | 20000224 |
| | JP 3124529 | B2 | 20010115 | | |
| | EP0710986-893331 | B2 | 19860331 | | |
| | US 1986-899344 | B2 | 19860822 | | |
| | US 1986-196660 | B2 | 19880520 | | |
| | JP 1098-258212 | B2 | 19881014 | | |
| | US 1986-839331 | B2 | 19860313 | | |
| | US 1987-56985 | A3 | 19870313 | | |
| | US 1987-281834 | A3 | 19870313 | | |
| | US 1989-347506 | A | 19890504 | | |
| | US 1989-US2169 | A | 19890518 | | |

AB A process for detg. the genotype of an individual with respect to the alleles at the HLA DP locus involves obtaining a sample of nucleic acid from the individual, and hybridizing the nucleic acids with a panel of probes specific for variant segments of DP α and DP β genes. Because the variation between DP β alleles is highly dispersed throughout the second exon of the DP β gene, the discovery of many different DP β alleles makes the process far more discriminating and informative than cellular RFLP, or serial methods. The process can also be carried out on amplified nucleic acid produced by the polymerase chain reaction using primers specific for the second exon of the DP α and DP β genes. HLA DP DNA typing methods are useful in the prevention of graft rejection and host vs. graft disease, in detg. susceptibility to autoimmune diseases, in providing evidence concerning the derivation from an individual of forensic samples, and in paternity testing.

IT 153032-04-3

RL: U.S. (Uses)

(Primer, for amplification of HLA DP α locus)

RN 153032-04-3 CAPLUS

CN DNA, 2(C-T-G-G-C-T-G-C-A-G-T-G-G-T-T-G-G-A-A-C-G-C) (9CI) (CA INDEX NAME)

NOTE singlestranded

SEQ: 1 ctaggtgcag tgggttggaa acgc

STN Columbus

L61 ANSWER 2 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1994:296653 CAPLUS

DN 120:296653

TI A method for preparing a kit for the detection of antibodies to HCV (hepatitis C virus) in biological samples such as blood serum

IN Houghton, Michael; Choo, Qui Lim; Kuo, George

PA Chiron Corp., India

SO Indian, 157 pp.

CODEN: INXXAP

DT Patent

LA English

FAN.CNT 8

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|----|---|------|----------|-----------------|--------------|
| PI | IN 171237 | A | 19920822 | IN 1990-CA801 | 19900917 |
| | AU 8927967 | A1 | 19890614 | AU 1989-27967 | 19881118 <-- |
| | AU 624105 | B2 | 19920604 | | |
| | ZA 8808669 | A | 19890830 | ZA 1988-8669 | 19881118 <-- |
| | BR 8807310 | A | 19900313 | BR 1988-7310 | 19881118 |
| | DD 287104 | A5 | 19910214 | DD 1988-321971 | 19881118 |
| | IN 169067 | A | 19910831 | IN 1988-CA960 | 19881118 |
| | DD 298524 | A5 | 19920227 | DD 1988-344401 | 19881118 |
| | DD 298525 | A5 | 19920227 | DD 1988-344402 | 19881118 |
| | DD 298526 | A5 | 19920227 | DD 1988-344403 | 19881118 |
| | DD 298527 | A5 | 19920227 | DD 1988-344404 | 19881118 |
| | CA 1373719 | A | 19930630 | CN 1992-110257 | 19881118 |
| | CA 1373719 | S | 20011107 | | |
| | JP 05091600 | A4 | 19931115 | JP 1989-500565 | 19881118 |
| | JP 05091644 | A2 | 19970715 | JP 1996-239921 | 19881118 |
| | JP 05091674 | A2 | 19980428 | JP 1997-99651 | 19881118 |
| | JP 05090696 | A2 | 19981104 | JP 1998-111631 | 19881118 |
| | JP 05090697 | A2 | 19981104 | JP 1998-111632 | 19881118 |
| | JP 0509023683 | A2 | 20000125 | JP 1999-157193 | 19881118 |
| | ES 2162894 | C2 | 20010210 | RU 1988-4742221 | 19881118 |
| | FI 8903447 | A | 19890717 | FI 1989-3447 | 19890717 <-- |
| | FI 105652 | B1 | 20000929 | | |
| | NO 8902931 | A | 19890913 | NO 1989-2931 | 19890717 <-- |
| | NO 804990 | B1 | 19990315 | | |
| | DK 8901537 | A | 19890718 | DK 1989-3537 | 19890718 <-- |
| | KR 136779 | B1 | 19980515 | KR 1989-701343 | 19890718 <-- |
| | KW 171238 | A | 19920822 | IN 1990-CA802 | 19900917 |
| | KW 171239 | A | 19920822 | IN 1990-CA805 | 19900917 |
| | IN 171240 | A | 19920822 | IN 1990-CA808 | 19900917 |
| | WO 9115771 | A1 | 19911017 | WO 1991-US2225 | 19910329 |
| | W: AU, BB, BG, BR, CA, FI, GB, HU, JP, KP, KR, LK, MC, MG, MW, NO, PL, RO, SD, SU | | | | |
| | RW: BF, BJ, CF, CG, CM, GA, ML, MR, SN, TD, TG | | | | |
| | AU 9176510 | A1 | 19911030 | AU 1991-76510 | 19910329 |
| | AU 639560 | B2 | 19930729 | | |
| | GB 2257784 | A1 | 19930120 | GB 1992-20480 | 19910329 |
| | BR 9106309 | A | 19930420 | BR 1991-6309 | 19910329 |
| | HU 52706 | A2 | 19930528 | HU 1992-3146 | 19910329 |
| | HU 217025 | B | 19991129 | | |
| | JP C5508219 | T2 | 19931118 | JP 1991-507636 | 19910329 |
| | JP 2733138 | B2 | 19980330 | | |
| | ES 109916 | B1 | 19950728 | RO 1975-92012 | 19910329 |
| | PL 172133 | B1 | 19970829 | PL 1991-296329 | 19910329 |

STN Columbus

| | | | | |
|---|----|----------|-----------------|----------|
| RU 2130969 | C1 | 19990527 | RU 1991-5053084 | 19910329 |
| EP 450931 | A1 | 19911009 | EP 1991-302910 | 19910403 |
| EP 450931 | B1 | 19960612 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| EP 693687 | A1 | 19960124 | EP 1995-114016 | 19910403 |
| EP 693687 | B1 | 19990728 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE | | | | |
| AT 139343 | E | 19960615 | AT 1991-302910 | 19910403 |
| ES 2088465 | T3 | 19960816 | ES 1991-302910 | 19910403 |
| AT 182684 | E | 19990815 | AT 1995-114016 | 19910403 |
| ES 2134388 | T3 | 19991001 | ES 1995-114016 | 19910403 |
| US 5683864 | A | 19971104 | US 1992-910760 | 19920707 |
| FI 106317 | B1 | 20010115 | FI 1992-4349 | 19920928 |
| NO 9203839 | A | 19921119 | NO 1992-3839 | 19921001 |
| NO 310241 | B1 | 20010611 | | |
| US 5714596 | A | 19980203 | US 1993-40564 | 19930331 |
| LV 10306 | B | 19950620 | LV 1993-442 | 19930531 |
| LV 10344 | B | 19960220 | LV 1993-4381 | 19930531 |
| US 5679342 | A | 19971021 | US 1993-97853 | 19930727 |
| US 5350671 | A | 19940927 | US 1993-103961 | 19930809 |
| LT 3808 | B | 19960325 | LT 1993-1747 | 19931230 |
| HR 940493 | B1 | 20001031 | HR 1994-940493 | 19940907 |
| US 5698290 | A | 19971216 | US 1994-306472 | 19940915 |
| US 6074816 | A | 20000613 | US 1994-307273 | 19940916 |
| US 5712087 | A | 19980127 | US 1995-440519 | 19950512 |
| US 6312399 | B1 | 20011106 | US 1995-440549 | 19950512 |
| US 5712098 | A | 19980127 | US 1995-440769 | 19950515 |
| US 6096541 | A | 20000801 | US 1995-441026 | 19950515 |
| US 6171782 | B1 | 20010109 | US 1995-442647 | 19950515 |
| US 6305412 | B1 | 20050301 | US 1995-441355 | 19950515 |
| US 6983219 | A | 19990126 | US 1995-472821 | 19950607 |
| NO 9503501 | A | 19951215 | NO 1995-5101 | 19951215 |
| NO 3904611 | B1 | 19991115 | | |
| NO 3504102 | A | 19951215 | NO 1995-5102 | 19951215 |
| NO 340410 | B1 | 19980914 | | |
| US 2000-62167 | A1 | 20030828 | US 1996-686983 | 19960725 |
| JP 09170079 | A2 | 19970708 | JP 1996-241451 | 19960822 |
| JP 0172793 | B2 | 20010604 | | |
| FI 9801380 | A | 19980615 | FI 1998-1380 | 19980615 |
| FI 106314 | B1 | 20010228 | | |
| GR 3031251 | T3 | 20000131 | GR 1999-402455 | 19990929 |
| PRAI US 1987-122714 | A | 19871118 | | |
| EP 1988-10A960 | A | 19881118 | | |
| US 1987-139886 | A | 19871230 | | |
| US 1988-161072 | A | 19880226 | | |
| US 1988-191263 | A | 19880506 | | |
| US 1988-263584 | A | 19881026 | | |
| US 1988-171450 | A | 19881114 | | |
| CN 1988-107988 | A | 19881118 | | |
| JP 1992-361785 | A3 | 19881118 | | |
| JP 1992-361787 | A3 | 19881118 | | |
| JP 1993-178446 | A3 | 19881118 | | |
| JP 1996-241451 | A3 | 19881118 | | |
| JP 1996-111631 | A3 | 19881118 | | |
| NO 1986-US4125 | A | 19881118 | | |
| US 1989-2138 | A6 | 19881118 | | |
| US 1989-325338 | B2 | 19890317 | | |
| US 1989-341334 | B2 | 19890420 | | |
| US 1989-353895 | B2 | 19890421 | | |
| US 1989-355002 | B2 | 19890518 | | |
| US 1989-355961 | B2 | 19890518 | | |
| NO 1989-2931 | A | 19890717 | | |

STN Columbus

| | | |
|----------------|----|----------|
| US 1989-398667 | B2 | 19890825 |
| US 1989-456637 | B2 | 19891221 |
| US 1990-504352 | A | 19900404 |
| US 1990-505435 | B2 | 19900404 |
| US 1990-566209 | B1 | 19900808 |
| US 1990-611965 | B2 | 19901108 |
| WO 1991-US2225 | A | 19910329 |
| EP 1991-302910 | A3 | 19910403 |
| US 1992-910760 | A3 | 19920707 |
| US 1993-40564 | A3 | 19930331 |
| US 1993-103961 | A1 | 19930809 |
| US 1994-306472 | A3 | 19940915 |
| US 1994-307273 | A3 | 19940916 |

AB The title kit contains a (recombinant) polypeptide contg. an HCV epitope, a pH buffer, a detection label, assay instructions, and packaging. Also provided are polynucleotide probes for detection of HCV nucleic acids, a monoclonal antibody to an HCV epitope for detection of HCV antigens by immunoassay, and vaccines comprising immunogenic peptides contg. an HCV epitope for treatment of HCV infections. The sequence of HCV cDNA suggests that HCV is or resembles a flavivirus. Thus, HCV was isolated from plasma of a chimpanzee with chronic non-A, non-B hepatitis and used to generate a λ-gt11 cDNA library which was screened for prodn. of epitopes which bound to serum from patients with non-A, non-B hepatitis. The cDNAs of several clones were sequenced and used to derive a composite sequence; the corresponding polypeptides were expressed in Escherichia coli as fusion products with superoxide dismutase.

IT 155182-96-8

RL: PNP (Properties)

(nucleotide sequence of)

RN 155182-96-8 CAPLUS

CN (hepatitis C virus polyprotein 128-amino acid fragment-specifying)
(OCL) (CA INDEX NAME)

SEQ: . . . ctggctgcgt ggtcatatgttggcagggtcg tcttgtccgg gaagccggca
50 acataacccgt acaggaaagt ctcttaaccgt gagttcgatg agatggaaaga
100 gtgtcttcgt cacttaccgt acatcgagca agggatgtatg ctcggcgagc
150 acatcaagca gaaggccctc ggcttcgtgc agaccgcgtc ccgtcaggca
200 gaggttatacg cccctgtctgt ccagatccaac tggcaaaaac tggagacatt
250 ctgggcgaag catatgtgga acttcatcg tgggatacaa tacttggcgg
300 ttgtgtcaac gtcgccttggt aaccccgcca ttgcttcatt gatggctttt
350 cggctgctg tcaccagccgt actaaccact agccaaa

L61 ANSWER IS OF 62. CAPLUS COPYRIGHT 2005 ACS on STN

FULL TEXT

AN 1991-306472 CAPLUS

DN 114:3793468

TI Cloning and analysis of the gene for the major outer membrane lipoprotein from *Pseudomonas aeruginosa*

AU Cornelis, P.; Bouia, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hanygaut, V.; Hubert, J. C.

CS Lab. Microbiol., Univ. Louis Pasteur, Strasbourg, 67070, Fr.

SO Molecular Microbiology (1989), 3(3), 421-8

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CCDEN: MOMIEE; ISSN: 0950-382X

DT Journal

LA English

AB The gene for the *P. aeruginosa* outer membrane lipoprotein I was isolated from a genomic library in the phage λ EMBL3 vector and subsequently

STN Columbus

subcloned in the low copy-no., wide host-range plasmid vector, pKT240. The cloned gene was highly expressed, resulting in the prodn. of a low mol.-wt. protein (8 kD) that was found to be assocd. with the outer membrane. Sequence anal. showed an open reading frame of 83 amino acids with a putative N-terminal hydrophobic signal peptide of 19 residues immediately followed by the lipoprotein consensus sequence, GLY-CYS-SER-SER (residues 19-22). The predicted amino acid compn. of the mature polypeptide and that of the purified lipoprotein I of *P. aeruginosa* were identical. In contrast with other Gram-neg. outer membrane lipoproteins, conformation predictions suggested that the mature protein was a single alpha helix.

IT 133020-34-5, Deoxyribonucleic acid (*Pseudomonas aeruginosa* clone

pLPII lipoprotein Opr I gene)

RL: PRP-(Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 133020-34-5 CAPLUS

CN DNA (*Pseudomonas aeruginosa* clone pLPII lipoprotein Opr I gene) (9CI) (CA INDEX NAME)

SEQ. 1 atgaacaacg ttctgaaatt ctctactctg gctctggctg ctgttctggc
51 caccgggtgc agcagccact ccaaagaac cgaagtcgt ctgaccgcta
101 ccgaagacgc agctgctcgat gtcaggctc gegetgacga agcttatcg
151 zaggctgacg aagctctggg cgctgcttag aaagctcagc agaccgctga
201 cgaggctaac gagctgtcccc tgctcatgt ggaaaaagcc agccgcaagt
251 aatacg

ANSWER 4 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

NAME: JEFFREY, JOHN

AU: 133020-3509 CAPLUS

CD: 133020-3509

TI: Cloning of gene for natriuretic and vasodilator peptide and its use for recombinant manufacture of these peptides

AV: Seifkher, J.; Jeffrey, John; Scarborough, Robert M.; Porter, J.; Gordon, J.

PA: California Biotechnology, Inc., USA

SD: PCT Int. Appl., 61 pp.

CODEN: PIXXD2

DT: Patent

LA: English

FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|----|---|------|----------|-----------------|----------|
| PT | WO 8912069 | A1 | 19891214 | WO 1989-US2373 | 19890531 |
| | W: AU, JP, KR, US | | | | |
| | EW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE | | | | |
| CA | 1330210 | A1 | 19970305 | CA 1989-601005 | 19890529 |
| AU | 8937681 | A1 | 19900105 | AU 1989-37681 | 19890531 |
| EP | 418308 | A1 | 19910327 | EP 1989-906935 | 19890531 |
| EP | 418308 | A1 | 19950816 | | |
| | R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE | | | | |
| JP | 03505280 | S2 | 19911121 | JP 1989-506595 | 19890531 |
| JP | 2511160 | S2 | 19960626 | | |
| US | 5114923 | A | 19920519 | US 1990-460855 | 19900202 |
| US | 5674710 | A | 19971007 | US 1990-477226 | 19900208 |
| US | 5949761 | A | 19990907 | US 1997-850910 | 19970505 |
| US | 6586396 | B1 | 20030701 | US 1999-287892 | 19990407 |
| US | 2003109430 | A1 | 20030612 | US 2001-902517 | 20010709 |
| US | 2004002458 | A1 | 20040101 | US 2003-402021 | 20030327 |

STN Columbus

| | | |
|---------------------|----|----------|
| PRAI US 1988-200383 | A | 19880531 |
| US 1988-206470 | A | 19880614 |
| US 1989-299880 | A2 | 19890119 |
| WO 1989-US2373 | A | 19890531 |
| US 1990-460855 | A | 19900202 |
| US 1990-477226 | A3 | 19900208 |
| US 1997-850910 | A3 | 19970505 |
| US 1999-287892 | A3 | 19990407 |

OS MARPAT 114:158509

AB The cDNA encoding prepro natriuretic peptide (NP) of porcine brain is cloned, sequenced, and used to clone the gene encoding natriuretic related peptide (NRP) from the genomic DNA of, e.g. pig, rat. From a porcine heart tissue cDNA library, an unprocessed cDNA encoding porcine brain natriuretic peptide (BNP) was cloned and sequenced. The cDNA clone (clone 14) contained at least an intron at residue Val22 of the 26-amino acid BNP (brain natriuretic peptide) and an upstream intron. Using clone 14 as a probe, the canine NRP-encoding gene was cloned and subcloned into plasmid pBR322 to obtain plasmid pdBNP-1, which was subsequently used to clone the human NRP gene.

IT 132444-45-2 132444-46-3 132444-48-5

RL: PRP (Properties)
(cloning of cDNA for and nucleotide sequence of)

RN 132444-45-2 CAPLUS

CN DNA, (swine brain natriuretic peptide-26 [Gly-9Ile-8Arg-7Ser-6Pro-5Lys-4Thr-3Met-2Arg-1]-specifying) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

RN 132444-46-3 CAPLUS

CN DNA, (swine brain natriuretic peptide-26 [Ser-6Pro-5Lys-4Thr-3Met-2Arg-1]-specifying) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

RN 132444-48-5 CAPLUS

CN DNA, (swine brain natriuretic peptide-26 [Thr-3Met-2Arg-1]-specifying) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

IT 122606-95-5, Deoxyribonucleic acid (pig brain natriuretic factor messenger RNA-complementary) 132444-47-4, Deoxyribonucleic acid

(pig brain natriuretic factor-26-specifying)

RL: PRP (Properties); BICL (Biological study)

(nucleotide sequence and cloning of)

RN 122606-95-5 CAPLUS

CN DNA (swine brain natriuretic peptide cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggcccccc ggatggcgctt tcccggttgtg ctccgtgtcc tggtttttgca
51 cgtgttgcgtg ctaggatggc gttcccatcc actgggtggc gtcggcctgg
101 cctcagaactt gcccaggata cagggatgtgc tggacccgcctt gggagacagg
151 gtctccggatc tgcaggccgg a cccggacggac tggagggccc tccggcagga
201 ccgtggccctc acagaaggct tggagggcgag ggaaggcagcc cccacgggggg
251 ttcttggggcc cccggatgtatcttccaag tccctccgggg aatacgcagc
301 cccaaaggacga tggatgtatc tggatgtgtttt gggcggaggc tggaccggat
351 cggatccctc agccggcctgg gctgcaatgt gtcaggagg tactga

RN 132444-47-4 CAPLUS

CN DNA (swine brain natriuretic peptide-26-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded

STN Columbus

SEQ 1 gactctggct gcttgggcg gagggctggac cggatcggt ccctcaggg
 51 cctgggctgc aatgtgctca ggaggtactg a

L61 ANSWER 5 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:494354 CAPLUS

DN 113:94354

TI Amyloid protein precursors, genetic probes, antibodies, and their use in diagnosis of Down's syndrome and Alzheimer's disease

IN Neve, Rachael L.

PA Children's Medical Center Corp., USA

SO PCT Int. Appl., 33 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT.1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|---|------|----------|-----------------|--------------|
| PI | WO 8907657 | A1 | 19890824 | WO 1989-US549 | 19890210 <-- |
| | W: AU, BR, DK, JP, KR
PW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE | | | | |
| | AU 8922046 | A1 | 19890906 | AU 1989-32046 | 19890210 <-- |
| PRAI | US 1988-154236 | A | 19880210 | | |
| | WO 1989-US549 | A | 19890210 | | |

AB A form of amyloid β -protein precursor DNA (designated APP-1) on chromosome 21 contains an exon encoding a polypeptide sharing significant homol. with Kunitz-type serine protease inhibitors. An alternate form (designated APP-2) lacks this exon, is expressed only in the brain, and has a pattern of distribution parallel to that of amyloid deposits in brains of patients with Alzheimer's disease and Down's syndrome. The exon is located at base pair 365 of APP-1 and interrupts the Val-289 codon of APP-1, changing it to an ile codon. The 2 forms, or their corresponding mRNA, are distinguished for diagnosis of the above diseases by selective hybridization, using a probe contg. the APP-2 Val-289 codon and subsegments on either side that hybridize to APP-2 nucleic acid but are too short to hybridize to APP-1 nucleic acid, and another probe contg. a sequence from the APP-1 exon long enough to hybridize to APP-1 nucleic acid. The corresponding polypeptides, contg. or not contg. the exon-encoded sequence, can be detected by use of specific antibodies for diagnosis of these diseases. The course of Alzheimer's disease and Down's syndrome involves a general decrease of APP-2 expression in affected areas of the brain, but a substantial increase in APP-1 expression in brain and regional tissue. Thus, a cDNA library was constructed from mRNA of human promyelocytic leukemia cell line HL60 and screened with FB68L, a fetal brain cDNA corresponding to the 3' portion of the APP gene, for probe selection. In a 19-wk Down's syndrome fetal brain, the hybridization of probes AMY3 (5'-CTGGCTGCTGTTGAGGAACCAACCTTCCACAGA-3') and HL124i (5'-ATGCAGTACTCTTCTGTCA-3') was greater than that to normal 19-wk fetal brain, indicating elevated levels of APP mRNA. In frontal cortex of Alzheimer's disease patients, expression of mRNA hybridizing to HL124i (i.e., contg. the exon-encoded sequence) was near normal, whereas that of mRNA hybridizing to AMY3 was markedly diminished.

IT 129766.91-2

RL: *TEST* (Analytical study)

{amyloid protein precursor 2 detection by hybridization with}

RN 129766-91-2 CAPLUS

CN DNA, d(C-T-G-G-C-T-G-C-T-G-T-T-A-G-G-A-A-C-T-C-G-A-A-C-C-A-C-C-T-T-T-C-C-A-C-A-G-A) (9CI) (CA INDEX NAME)

STN Columbus

NTE singlestranded

SEQ 1 ctggctgctg ttgttaggaac tcgaaccacc tttccacaga

L61 ANSWER 6 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:453375 CAPLUS

DN 113:53375

TI Secondary structure of 7SK and 7-2 small RNAs. Possible origin of some 7SK pseudogenes from cDNA formed through self-priming by 7SK RNA

AU Suh, Dick; Yuan, Yan; Henning, Dale; Reddy, Ram

CS Dep. Pharmacol., Baylor Coll. Med., Houston, TX, 77030, USA

SO European Journal of Biochemistry (1989), 186(1-2), 221-6

CODEN: EJBCAI; ISSN: 0014-2956

DT Journal

LA English

AB Pseudogenes having homol. to small RNAs, like 7SL, 7SK, 6S, 4.5S, U1, U2, and U3 RNAs, are abundant and dispersed in the genomes of higher eukaryotes. To better understand the possible origin of these pseudogenes, the abilities of cytoplasmic 7SL, 7SK, and nucleolar 7-2 RNAs to self-prime and result in the synthesis of cDNAs were studied. When rat 7SK RNA was used as substrate, a 294-nucleotide-long cDNA was synthesized in vitro by reverse transcriptase, indicating that the 3' end of 7SK RNA can act in a self-priming manner to generate 7SK cDNA. When 7-2 RNA was used as a substrate, a cDNA of approx. 235 nucleotides was obsd.; 7SL RNA did not act as a self-primer. Earlier studies have shown that DNAs homologous to 7SK RNA are represented by a moderately reiterated family in the mammalian genomes and many of these sequences were found to be truncated 7SK pseudogenes. In this study, one 7SK clone from the rat genome was characterized by sequencing. This clone contained 243 base pairs homologous to the 5' end of 7SK RNA, and was flanked by direct repeats. These data suggest that, as previously proposed for some U3 pseudogenes, one mechanism for the generation of truncated 7SK pseudogenes may be the integration of self-primed reverse transcripts of 7SK RNA at random genomic sites.

FT 128283-72-7, Deoxyribonucleic acid (rat Nouikoff cell clone 7SK-1 7-3 RNA pseudogene)

RL PRP (Properties); BIO (Biological study)
(nucleotide sequence of)

RN 128283-72-7 CAPLUS

CM DNA (rat Nouikoff cell clone 7SK-1 7-3 RNA pseudogene) (9CI) (CA INDEX)
NAME

SEQ 1 gactttcaat caacaaatgg ggatgtgagg ggcgatctggc tggcgacatct
51 atcaccatccat tgatgccac ggttggattcg gctgatctcg ctggcttaggc
101 ggggtgtcccc atcccccctc accgctccat gtgcgtccct cccgaagctg
151 cgcgctcggt cggaaaggac gaccttcccc gaatacgagga ggacgggtct
201 tcggtaagg gtatacgagt agctgcgcctc ccctgctaga acctccaaac
251 aagctctcaa tgtaatcaa caaatggcca tcaacaaaac aaattcaatg
301 g

L61 ANSWER 7 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:437392 CAPLUS

STN Columbus

DN 113:37392
 TI Sex determination in ruminants using Y-chromosome-specific polynucleotides and isolation and sequencing of Y-chromosomal DNA repeat
 IN Reed, Kenneth Clifford; Lord, Eric Arthur; Mattheai, Klaus Ingo; Mann, David Andrew; Beaton, Sandra; Herr, Charles Marvin; Matthews, Margaret Ellen

PA Advanced Riverina Holdings Ltd., Australia

SC PCT Int. Appl., 120 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|---|------|----------|-----------------|--------------|
| PI | WO 8907154 | A1 | 19890810 | WO 1989-AU29 | 19890127 <-- |
| | W: AU, JP, US
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE | | | | |
| | AU 8930451 | A1 | 19890825 | AU 1989-30451 | 19890127 <-- |
| | AU 628800 | B2 | 19920924 | | |
| | EP 397753 | A1 | 19901122 | EP 1989-902001 | 19890127 |
| | EP 397753 | B1 | 19960612 | | |
| | R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE | | | | |
| | JP 03503358 | T2 | 19910801 | JP 1989-501848 | 19890127 |
| | AT 139265 | E | 19960615 | AT 1989-902001 | 19890127 |
| | US 5459038 | A | 19951017 | US 1993-175679 | 19931230 |
| PRAI | AU 1988-6476 | A | 19880129 | | |
| | WO 1989-AU29 | A | 19890127 | | |
| | US 1090-548903 | B1 | 19900927 | | |
| | US 1095-3695 | B1 | 19930113 | | |
| RE | Nucleic acids capable of hybridizing only to Y-chromosome-specific DNA sequences of ruminants are isolated and their sequences disclosed. A method of detg. sex of ruminants using polymerase chain reaction (PCR) method is also given. Thus, Y-chromosomal DNA repeats OY1.1 (3142 bp), OY4.1 (2552 bp), OY4.2 (1076 bp), OY9.2-9.5 (8010 bp), OY 11.1 (3983 bp), BRY4b (4189 bp), and BRY4c (4201 bp) of sheep; GRY.1a(a) (384 bp) and GRY.1b(a) (448 bp), as well as GRY1a and GRY1b (2589 bp) of goats; and BRY.1c(d) (545 bp) and BRY.4c(i) (484 bp) of cattle were isolated from the resp. ruminant liver cell genomic library using radioactive, Y-chromosome-specific probe DNA such as BRY1 or OY11.1. The ruminant DNA repeats were subsequently detd. Genetic sexing of bovine embryos using PCR was exemplified wherein the presence of a 130-bp PCR product upon gel-electrophoresis was used as male criteria. | | | | |
| IT | 128151-31-5, Deoxyribonucleic acid (goat clone λ-CGY1 male-specific GRY.1a(a) element) | | | | |
| RL | PRP (Properties)
(nucleotide sequence of) | | | | |
| RN | 128151-31-5 CAPLUS | | | | |
| CN | DNA (goat clone λ-CGY1 male-specific GRY.1a(a) element) (9CI) (CA INDEX NAME) | | | | |
| MFE | double stranded | | | | |
| SEQ | 1 acaactcaca gatttgacag actgcgaggc cctgggagtg tgacacttgc
51 atatgtgacac tgcagctgga agggagtagg aaactggcg ggccgcgtgtct
101 ggccgggtgt gtggtttttc cagctgtcac ctctctgcct ctcagaatttcc
151 aatatggcgct tcatagtgatt cataaaacttg acatttttta gaactttcaa
201 ccggctgtgagg catttaaacg ctgtgtgggt cttcgtttct ggctgccccaa
251 ctcctataag ctctccatag tagaagtacg gaagtacaca atcagatttc
301 cttctgtggg atcaacaatc ttgtttggac ttgtctaaact tgaaaaatca
351 gtttttgtca gtccatttttc ccctaaaggt ctca | | | | |

STN Columbus

gave the structure of the entire 3' untranslated region, a coding region corresponding to winter flounder MT, and 49 nucleotides of the 5' untranslated region. One of the flounder MT cDNAs, pWFMTC4, was subcloned into a RNA probe plasmid and transcribed to produce antisense MT RNA (cRNA). The MT cRNA was then used to detect the induction of MT mRNA (prodn. in the liver of winter flounder, following the administration of Cu²⁺, Zn²⁺, Cd²⁺, Pb²⁺ and Hg²⁺. The time required for the induction of hepatic MT mRNA by a single injection of Cd²⁺ was approx. 96 h. Dexamethasone did not induce an increase of MT mRNA in any of the winter flounder tissues examd. (liver, kidney, heart, brain, intestinal scrape, and gill filament), whereas Cd²⁺ induced MT mRNA in all of the tissues except brain, where the constitutive level of expression was high.

IT 127385-13-1, Deoxyribonucleic acid (Pseudopleuronectes americanus clone pWFMTC69 metallothionein messenger RNA-complementary)
 RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)
 RN 127385-13-1 CAPLUS
 CN DNA (Pseudopleuronectes americanus clone pWFMTC69 metallothionein cDNA)
 (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 a:ggatccct gcgaatgctc caagacttggaa acctgcaact gcccggggatc
 51 ttgcacccgc aagaactgca gtcgcaccac ctgcacaacaa agctgtgtcc
 101 cttgtgtcccc atccggctgc cccaaatgtcgat cctctggctg cgttgtcaaa
 151 gggaaagacat ggcacaccac ttgtgtcaag tga

L61 MSGWAN 10 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

EP21 Jank
 AN 1996-03-1555 CAPLUS
 DN 112-011-55
 TI Nucleotide sequences from the colicin E5, E6 and E9 operons: presence of a degenerate transposon-like structure in the ColE9-J plasmid
 AU Lau, Peter C. K.; Condie, Janet A.
 CS Biotechnol. Res. Inst., Natl. Res. Coun. Canada, Montreal, QC, H4P 2R2, Can.
 SO Molecular and General Genetics (1989), 217(2-3), 269-77
 =====

CODEN: MGGEAE; ISSN: 0026-8925

DT Journal
 LA English
 AB The nucleotide sequences of 1288 bp of plasmid ColE5-099, 1609 bp of ColE6-CT14, and 2099 bp of ColE9-J were detd. These sequences encompass the structural gene for the C-terminal receptor-binding and nuclease domain of colicins E5, and E6, and E9, their cis- or trans-acting immunity proteins and four lysis proteins, including an atypical one of non-lipoprotein nature (Lys*) present in the ColE9-J plasmid. The ColE6 gene organization, in the order col-imm-E8imm-lys, is identical to that found in the double-immunity gene system of ColE3-CA38 (an RNase producer). The corresponding genes in the two plasmids are 87%-94% homologous. In ColE9-J, the genes are organized as col-imm-lys*-E5imm-lys. The E9 col-imm gene pair is homologous to the colicin E2-P9 type (a DNase producer). Downstream from E9imm is an E5imm (designated E5imm[E9]) which is trans-acting. Neither the predicted structures of E5Imm[E9] nor the cis-acting Imm resident in the ColE5-099 plasmid which differs by a single amino acid shows any resemblance to other immunity structures which have been sequenced. Furthermore, the E5cl sequences differ from those previously for other colicins except for the conserved btuB-specified receptor-binding domain. A novel 205 nucleotide long insertion sequence

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is found in the ColE9-J plasmid. This insertion sequence, which was named ISE9, has featured reminiscent of the degenerate transposon IS101 found in plasmid pSC101. One effect of ISE9 is the presence of the atypical lysis gene, lys*. The presence of a transposon-like element in the ColE9 plasmid exemplifies a new phenomenon relevant to the evolution of colicin E plasmids.

IT 126547-55-5, Deoxyribonucleic acid (plasmid ColE6-CT14 gene lys)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)
RN 126547-55-5 CAPLUS
CN DNA (plasmid ColE6-CT14 clone pAM362 gene lys) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaaaaaa taacaggat tattttattt cttcttcgcag tcattattct
51 ggctgcgtgt caggcaact atatccgtga tgttcaggc ggactgtat
101 caccgtcgta aactgctgaa ctgaccggag tggaaacgca gtaa

L61 ANSWER 11 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:193120 CAPLUS
DN 112:193120
TI Production and engineering of human lysozyme using recombinant DNA techniques
AU Muraki, Michiro; Jigami, Yoshifumi; Tanaka, Hideaki
CS Natl. Chem. Lab. Ind., Tsukuba, Japan
CO Kagaku Gijutsu Kenkyusho Hokoku (1989), 84(8), 495-501

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CODEN: KCKHEP; ISSN: 0388-3213

DT Journal

LA Japanese

AB An artificial gene encoding human lysozyme was chem. synthesized and expressed both in Escherichia coli and Saccharomyces cerevisiae. The product in E. coli formed insol. aggregates and had no enzymic activity. Urea treatment of the aggregates regenerated the enzymic activity partly, but the yield was very low. To examine the extracellular prodn. of human lysozyme by S. cerevisiae, the signal peptide gene of chicken lysozyme was fused to the 5'-end of the mature human lysozyme gene. The S. cerevisiae cells harboring the chimeric prelysozyme gene secreted the enzymically active human lysozyme into the culture medium. A single chromatog. with a cation exchanger gave an almost pure enzyme with an identical specific activity to that of the authentic human lysozyme. The identity of the N-terminal amino acid sequence of the purified enzyme compared with that of authentic human lysozyme indicated correct processing of the chicken signal peptide and the successful prodn. of human lysozyme occurred in S. cerevisiae cells. Amino acid residues composing the catalytic cleft of human lysozyme were changed by site-specific mutagenesis. Conversions of catalytic residues, Glu-35 to Asp and/or Asp-53 to Glu, remarkably decreased the enzymic activity, reflecting the fragility of the catalytic site. Mutagenesis of the three arom. residues which are conserved among the same type lysozymes revealed that an arom. residue at position 63 and a tryptophan at 64 were crucial for the recognition of substrates. On the other hand, a tryptophan at 109 was essential for the efficient cleavage of the substrate, but not for the substrate recognition. Modification of the charge state of the residue at 115 changed the cleavage pattern of an oligosaccharide substrate, N-acetylglucosamine pentamer, suggesting the possibility of the artificial alteration of products in the enzymic reaction. The effect of the change in surface charge of the enzyme was also examd. The mutant human lysozymes with an increased or a decreased

STN Columbus

pos. charge showed higher lytic activity than the wild-type enzyme under conditions not optimal for the wild-type enzyme in regard to the ionic strength and pH. These results demonstrate the effectiveness of a protein engineering approach in improving the protein function as well as in elucidating the structure-function relationships of proteins.

IT 126627-25-6P, Deoxyribonucleic acid (chicken prelysozyme signal peptide-specifying)

RL: PREP (Preparation)

(prepn. of, for lysozyme synthetic gene cloning)

RN 126627-25-6 CAPLUS

CN DNA (chicken prelysozyme signal peptide-specifying) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 tcgactcgat gaggtctttg ctaatcttgg tgctttgttt cctgccccctg
51 gctgctctgg ggaaggttt

1 cggaaacctt ccccaagagca gccaggggca ggaagcaaag caccaggatt
51 agcaaagacc tcatcgag

L61 ANSWER 12 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:173112 CAPLUS

DN 112:173112

TI Molecular structure and immunity specificity of colicin E6, an evolutionary intermediate between E-group colicins and cloacin DF13

AU Akagi, Akiko; Masaki, Haruhiko; Ohta, Takahisa

OS Dep. Agric. Chem., Univ. Tokyo, Tokyo, 113, Japan

SP JOURNAL OF BACTERIOLOGY (1989), 171(12), 6430-6

CODE: JBBAY; ISSN: 0021-9193

BY Colicin

Enzyme

The primary structure of a 3.1-kilobase E6 or E3 segment carrying colicin and related genes was detd. Plasmid ColE6-CT14 showed striking homol. to ColE6-CA38 throughout this segment, including homol. to the secondary immunity gene, immE8, downstream of the E6 or E3 immunity gene. The ColE6-CA38 and ColE6-CT14 sequences, however, contained an exceptional hot spot region encoding both the colicin-active domain (RNase region) and the immunity protein, reflecting their different immunity specificities. On the other hand, some chimeric plasmids were constructed through homologous recombination between colicin E3 and cloacin DF13 operons. The resulting plasmids were deduced to produce chimeric colicins with a colicin E3-type N-terminal part, a cloacin DF13-type C-terminal-active domain, and the DF13 immunity protein. The killing spectra of the chimeric colicins and the immunities of the plasmids were identical to those of colicin E6 and ColE6-CT14, resp., showing that the colicin E6 immunity specificity is completely equiv. to that of cloacin DF13. Nevertheless, colicin E6 has been found to show a sequence diversity from cloacin DF13 almost to the same extent as that from colicin E3 in their RNase and immunity regions, indicating that only a small no. of amino acids defines the immunity specificity for discrimination between colicins E3 and E6 (or cloacin

IT 126627-54-5, Deoxyribonucleic acid (plasmid ColE6-CT14 clone pAM362 gene lys)

RL: PROPS (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 126627-55-5 CAPLUS

CN DNA (plasmid ColE6-CT14 clone pAM362 gene lys) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

SEQ 1 atgaaaaaaaaaa taacagggat tatttttattt cttcttcgcag tcattattct
51 ggctgcgtatgt caggcaact atatccgtga tgttcagggc gggactgtat
101 caccgtcgta aactgctgaa ctgaccggag tggaaacgca gtaa

L61 ANSWER 13 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:152605 CAPLUS

DN :112:152605

TI Multiple copies of the coding regions for the light-harvesting B800-850 α - and β -polypeptides are present in the Rhodopseudomonas palustris genome

AU Tadros, Monier Habib; Waterkamp, Karin
CS Inst. Biol., Freiburg, D-7800, Fed. Rep. Ger.

SO EMBO Journal (1989), 8(5), 1303-8

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CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB A reverse-phase HPLC System for isolation of the water insol. α - and β -polypeptides of the light-harvesting complex II (LH II) of R. palustris without employment of any detergent was developed. The material obtained was of high purity and suitable for direct microsequence anal. Chromatog. anal. could resolve ≥ 2 major β -polypeptides, $\beta\alpha$ and $\beta\beta$, 2 major α -polypeptides, $\alpha\alpha$ and $\alpha\beta$, and 5 addnl. minor polypeptides. N-terminal acid sequencing shows that the measured peaks correspond to different polypeptide species, and that the minor species have an N-terminal sequence identical to that of the α 1 polypeptide. An oligonucleotide derived from the N-terminal sequence of the α 2 polypeptide was utilized to screen a genomic library from R. palustris. Several independent clones were characterized by Southern blot and nucleotide sequence anal. R. palustris contains 23 different clusters of β and α genes. Two clones contain sequences potentially coding for $\beta\alpha$ - $\alpha\alpha$ and $\beta\beta$ - $\alpha\alpha$ polypeptides; and 2 addnl. clones potentially coding for β and α peptides which were named β c- α c and β d- α d, which did not correspond to the major purified polypeptides. In addnl. to the protein chem. data, the conservation at the amino acid level and the presence of canonical ribosomal binding sites upstream of each of the identified genes strongly suggest that all 4 coding regions are expressed.

IT 125858-45-8, Deoxyribonucleic acid (Rhodopseudomonas palustris clone vphi.-4 light-harvesting protein B 800-850 β isoform a gene)

125858-47-1, Deoxyribonucleic acid (Rhodopseudomonas palustris clone vphi.-6 light-harvesting protein B 800-850 β isoform b gene)

125858-51-7, Deoxyribonucleic acid (Rhodopseudomonas palustris clone vphi.-1 light-harvesting protein B 800-850 β isoform d gene)

RA: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 125858-45-9 : CAPLUS

CN DNA (Rhodopseudomonas palustris clone vphi.-4 light-harvesting protein B 800-850 β isoform a gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggctgaca agacgctgac cggcctgacg gtcgaggagt ccgaagagct
51 ccaczaagcac gtgatcgatg gcacccgcat ttccgtgcg atcgcgatcg

STN Columbus

101 tcgcgcactt cctcgccatc gtttactcgc cctggctgca cttaa

RN 125858-47-1 CAPLUS

CN DNA (Rhodopseudomonas palustris clone .vphi.-6 light-harvesting protein B
800-850 β isoform b gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggcagacg atccgaacaa ggtctggccg accggctctga cgatcgccga
51 atcggaaagag ctccacaagg atgtgatcga cggcacgcgc attttcggcg
101 cgatcgccat cgtcgctcac ttcttggcgt atgtttattc gccctggctg
151 cactaa

RN 125858-51-7 CAPLUS

CN DNA (Rhodopseudomonas palustris clone .vphi.-1 light-harvesting protein B
800-850 β isoform d gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggtagacg atccgaacaa ggtctggccg actgggctga ccatcgccga
51 atcggaaagag ctccacaagg acgtgatcga tggttcgcgg attttcgtgg
101 ccatcgccat cgtggcgcat ttcttggcgt acgtttactc gccctggctg
151 cactaa

LSI ANSWER 24 OF 52 CAPLUS. COPYRIGHT 2005 ACS on STN

Full Text

AN 1090:133420 CAPLUS

DN 112:133430

TI Isolation and structural characterization of cDNA clones encoding the
mating pheromone Er-1 secreted by the ciliate Euplotes raikovi

AU Miceli, Cristina; La Terza, Antonietta; Melli, Marialuisa

CS Dep. Cell. Biol., Univ. Camerino, Camerino, 62032, Italy

SO Proceedings of the National Academy of Sciences of the United States of
America (1989), 86(9), 3016-20

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CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB CDNA clones comprising the entire coding region for the mating pheromone
Er-1 of E. raikovi were isolated by oligonucleotide screening of two cDNA
libraries in the vectors λgt10 and pUC12. The cDNA sequence
contains an open reading frame of 75 amino acids that constitute
pre-pro-Er-1. The amino acid sequence of secreted Er-1 starts at aspartic
acid-39 of pre-pro-Er-1 and completely matches that known by direct Er-1
protein sequencing. The coding region of Er-1 cDNA ends with codon TAA,
which specifies glutamine in other ciliates. The 5'- and 3'-noncoding
regions contain, resp., two and one inverted repeats. The
3'-noncoding-region inverted repeat, which includes the unusual
polyadenylation signal AACAAA, has been related to RNA 3'-terminus
formation.

IE 125546-74-9; Deoxyribonucleic acid (Euplotes raikovi clone
λ4/p3/5b euplomone r 1 messenger RNA-complementary)

RL PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 125546-74-9 CAPLUS

STN Columbus

CN DNA (Euplotes raikovi clone λ4/p3/5b euplomone r 1 cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaacaaac tagcaattct cgctatcatc gctatggta ctttcagcgc
51 caacgccttc agattccaaa gcagatttagt atcaaatgt aagactaaga
101 caggagatgc ttgtgagcaa gctgcaatcc agtgtgttga gtcagcatgt
151 gaaagtcttt gtacagaagg tgaagataga actggctgt atatgtacat
201 ctattctaact gcccacccat atgtctaa

L61 ANSWER 15 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:133303 CAPLUS

DN 112:133303

TI Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning, sequence, and expression in Escherichia coli

AU Duhéne, Michael; Barron, Carlos; Schweizer, Andrea; Von Specht, Bernd Ulrich; Domdey, Horst

CS Lab. Mol. Biol., Ludwig-Maximilians-Univ. Muenchen, Martinsried, D-8033, Fed. Rep. Ger.

SC Journal of Bacteriology (1989), 171(8), 4130-7

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AP Lipoprotein I (OprI) is one of the major proteins of the outer membrane of *Pseudomonas aeruginosa*. Like porin protein F (OprF), it is a vaccine candidate because it antigenically cross reacts with all serotype strains of the International Antigenic Typing Scheme. Since lipoprotein I was expressed in *Escherichia coli* under the control of its own promoter, it was possible to isolate the gene by screening a (λ) EMBL3 phage library with a mouse monoclonal antibody directed against lipoprotein I. The monocistronic OprI mRNA encodes a precursor protein of 83 amino acid residues, including a signal peptide of 19 residues. The mature protein has a mol.wt. of 6950, not including bound glycerol and lipid. Although the amino acid sequences of protein I of *P. aeruginosa* and Braun's lipoprotein of *E. coli* differ considerably (only 30.1% identical amino acid residues), the sequences at the signal peptidase cleavage site and at the C terminus, which is the attachment site to peptidoglycan in *E. coli*, are identical. Using lipoprotein I expressed in *E. coli*, it can now be tested whether this protein alone, without *P. aeruginosa* lipopolysaccharide contaminants, has a protective effect against *P. aeruginosa* infections.

IT 125323-B4-2 Deoxyribonucleic acid (*Pseudomonas aeruginosa* clone

pITaqI lipoprotein I gene)

PR (Properties); BIOC (Biological study)

(nucleotide sequence of)

RN 125723-82-2 CAPLUS

CN RNA (*Pseudomonas aeruginosa* clone pITaqI lipoprotein I gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaacaaac ttctgaaatt ctctyctctg gctctggctg ctgttctggc
51 caccgggttgc agcagccact ccaaagaaac cgaagctcgat ctgaccgcata
101 ccgaagacgc aycgtctcgat gtcaggctc ggcgtacgaa agctatcg
151 aaygtccacq aagctctggg cgtctcgat aaagctcagc agaccyctga
201 cgaggctaac gagegtgccccc tgccatgtct ggaaaaagcc agccgcaagt

STN Columbus

251 aa

L61 ANSWER 16 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:71242 CAPLUS

DN 112:71242

TI Nucleotide sequences of *Caenorhabditis elegans* core histone genes. Genes for different histone classes share common flanking sequence elements

AU Roberts, Susan Boseman; Emmons, Scott W.; Childs, Geoffrey

CS Dep. Genet., Albert Einstein Coll. Med., Bronx, NY, 10461, USA

SO Journal of Molecular Biology (1989), 206(4), 567-77

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CODEN: JMOBAK; ISSN: 0022-2835

DT Journal

LA English

AB The nucleotide sequence of core histone genes and flanking regions from 2 of approx. 11 different genomic histone clusters of the nematode *C. elegans* were detd. Four histone genes from one cluster (H3, H4, H2B, H2A) and 2 histone genes from another (H4 and H2A) were analyzed. The predicted amino acid sequences of the two H4 and H2A proteins from the 2 clusters are identical, whereas the nucleotide sequences of the genes have diverged 9% (H2A) and 12% (H4). Flanking sequences, which are mostly not similar, were compared to identify putative regulatory elements. A conserved sequence of 34 base pairs is present 19 to 42 nucleotides 3' of the termination codon of all the genes. Within the conserved sequence is a 16-base dyad sequence homologous to the one typically found at the 3' end of histone genes from higher eukaryotes. The *C. elegans* core histone genes are organized as divergently transcribed pairs of H3-H4 and H2A-H2B and contain 5' conserved sequence elements in the shared spacer regions. One of the sequence elements, 5'-CTCCNCCTNCCCACNCANA-3', is located immediately upstream from the canonical TATA homol. of each gene. Another sequence element, 5'-CGCGCGGACACATNT-3', is present in the spacer of each geneotypic pair. These two 5' conserved sequences are not present in the promoter region of histone genes from other organisms, where 5' conserved sequences are usually different for each histone class. They are also not found in non-histone genes of *C. elegans*. These putative regulatory sequences of *C. elegans* core histone genes are similar to the regulatory elements of both higher and lower eukaryotes. The coding regions of the genes and the 3' regulatory sequences are similar to those of higher eukaryotes, whereas the presence of common 5' sequence elements upstream from genes of different histone classes is similar to histone promoter elements in yeast.

BT 125122-13-6, Deoxyribonucleic acid (*Caenorhabditis elegans* clone

pCeh-1 gene his-3)

AB: PRF (Properties): BIOL (Biological study)

(nucleotide sequence of)

RN 125122-13-6 CAPLUS

GN DNA (*Caenorhabditis elegans* clone pCeh-1 gene his-3). (9CI) (CA INDEX NAME)

WT doublestranded

SEQ 1 atgtctggac gcgaaaggg aggcaaagcc aagaccggag gaaaggccaa
51 gtccccctca tcaagagccg yactccaatt cccagtttgt cgtttcacc
101 gtattctccg taaaaggaaac tacgtcaac gtgttggagc cgagccccca
151 gtttacctgg ctgcgcgttct tgagtacctc gctgctgagg ttctcgagtt
201 ggctggaaac gtcgcgcgtg ataacaagaa gaccagaatt gccccaagac
251 atctccaact ggccgcgttct aacgtatggg agttgaacaa actgttggt
301 ggagtaacca tcgccccagg aggagttctt ccaaataatcc aagctgttct

STN Columbus

351 tttgccaaag aaaaccggag gagacaaggaa atag

L61 ANSWER 17 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1990:17045 CAPLUS

DN 112:17045

TI Structure and evolution of somatostatin genes

AU Su, Chung Jey; White, James W.; Li, Wen Hsiung; Luo, Chi Cheng; Frazier, Marsha L.; Saunders, Grady F.; Chan, Lawrence

CS Syst. Cancer Cent., Univ. Texas, Houston, TX, 77030, USA

SO Molecular Endocrinology (1988), 2(3), 209-16

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CODEN: MOENEN; ISSN: 0888-8809

DT Journal

LA English

AB A bovine pancreatic preprosomatostatin cDNA clone was isolated and sequenced. Although it encodes a predicted 116-amino acid preprosomatostatin that is very similar in primary structure to those deduced from other mammalian preprosomatostatin cDNAs, there are some differences in amino acid compn. Hybridization of this clone to Northern blots of fetal bovine pancreatic poly(A)+ RNA reveals a mRNA of 700 nucleotides. Evolution of the preprosomatostatin genes was studied by statistical anal. of anglerfish, catfish, bovine, rat, and human cDNA sequences. The results suggest that the 2 somatostatin genes present in both anglerfish and catfish were the result of a gene duplication event in a common ancestor of anglerfish and catfish.

IR 124363-90-2, Deoxyribonucleic acid (ox clone FBPS-2 somatostatin messenger RNA-complementary)

RL RN (Properties); BIOL (Biological study)
(nucleotide sequence of)

AN 124363-90-2 CAPLUS

CN DNA (cattle clone FBPS-2 somatostatin cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded.

SEQ

1-
51-
101-
151-
201-
251-
301-
351-

gtgtgtctt gccgcctcca gtgcgcgtg gcccgcgtct ccatcgcc
ggctcttggc ggtgtcaccc ggcgcgcctc ggatccccgg ctccgtcagt
tgtcagaa atccctggct gtcgcgcgtg gcaaggcaggaa actggccaa
tacttcttgg cagagctgtc gtgtgaaccc aaccagacag agattgtatgc
ctggagactt gaaattttgt cccaggctgc tgagcaggat gaaatgaggc
tggagctgca gagatctgtc aactcaaacc cggccatggc accccgagaa
ggcaaaatgtc gtgtcaagaa ttctttctgg aagactttca catcctgtta

L61 ANSWER 18 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:547785 CAPLUS

DN 111:147785

TI Nucleotide sequence of cDNA for rat liver and brain cytochrome c oxidase subunit VIa (Vb)

AU Goto, Yoshitaka; Amuro, Nacki; Okazaki, Taro

CS Dep. Biochem., Nippon Med. Sch., Tokyo, 113, Japan

SO Nucleic Acids Research (1989), 17(15), 6388

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CODEN: NARHAD; ISSN: 0305-1048

DT Journal

STN Columbus

LA English
AB The nucleotide sequence of the cDNA for cytochrome c oxidase [EC 1.9.3.1] subunit VIa (Vb) from rat liver is reported. The cDNA insert of the liver was 434 bp, contg. a 5'-untranslated region of 54 bp, a coding region of 297 bp, a 3'-untranslated region of 83 bp and a poly(A) tail. The deduced amino acid sequence is composed of 99 residues, including the amino terminal methionine, and differs from the amino acid sequence of bovine heart mature subunit VIa by 17 out of 98 residues. Since the nucleotide sequence of rat brain cDNA was found to be completely identical with that of liver, it is assumed that the same gene is expressed in both the liver and brain of rat.

IT 123008-93-5, Deoxyribonucleic acid (rat liver cytochrome oxidase subunit VIa messenger RNA-complementary)
RL: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)
RN 123008-93-5 CAPLUS
CN DNA (rat liver cytochrome oxidase subunit VIa cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggcttctg gaggtgggtgt ccctactgtat gaggaggcagg ctaccgggct
51 ggagaggag atcatgatag cagcacagag gggactggat ccatacaata
101 tgcacccccc aaaggcagct tcggycacca aggaagaccc caatcttagtc
151 ccatccgta gcaacaagag aatagtgggc tgcacatctgtg aagaggacaa
201 ctgcactgtc atctgggtct ggctgcacca aggcgagagc cagcgatgcc
251 ccaactgtgg aacacattac aagtgggtgc octaccaaat ggtccactga

LSI1 JOURNAL 19 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

AN 1989-562169 CAPLUS
ID 1A1-122169

AB A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.
AU Brown, Keith D.; Zurawski, Sandra M.; Mosmann, Timothy R.; Zurawski, Gerard
CS Res. Inst. Mol. Cell. Biol., DNAX, Palo Alto, CA, 94304, USA
SO Journal of Immunology (1989), 142(2), 679-87

COPIN: JOIMA3; ISSN: 0022-1767

DT Journal
LA English

AB Four cDNA clones that encode mRNA expressed more abundantly in Con A-activated mouse helper T cells than by resting T cells were isolated and characterized. One mRNA encoded a ~14-kDa protein with a hydrophobic N-terminal sequence and was abundantly expressed by the Th 2 subset of T-helper (Th) cells, but was not expressed by Th 1 cells. The remaining 3 mRNA encoded related ~8-kDa secreted proteins that are part of a family of small, secreted, and inducible mouse and human proteins. This family of proteins is itself distantly related to another family of growth and inflammatory factors that are assocd. with various lymphoid and fibroblast activation phenomena. One of the small, inducible, secreted proteins has a predicted mature N terminus identical to that of the previously described macrophage inflammatory protein.

IT 123009-54-4, Deoxyribonucleic acid (mouse clone P500 protein SIS isoform messenger, RNA-complementary)
RL: PRP (Properties)
(nucleotide sequence of)

STN Columbus

RN 122783-54-4 CAPLUS
CN DNA (mouse clone P500 protein SIS α -isoform cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaccca ctggccatggc actgatgtgc ctgtctgtgg ctggccgtgtg
51 gatacaggat gttgacagca aga \bar{g} catgtct tacyggcttcc aatagtcgtct
101 gcttgaaacac cttgaagaaa gagttcccc tgaagtttat ccagtgttac
151 agaaaagatgg gctccttcctg tcctgatccc ccagctgtgg tagtcaggag
201 ttcaggggtc cctggctca cagaaggcaga gaagactgtt acagattcca
251 gtgagtga

L61 ANSWER 20 OF 62 CAPLUS COPYRIGHT 2005 ACS cn STN

Full Text

AN 1989:491439 CAPLUS

DN 113:91439

MI Cloning and sequence analysis of cDNA encoding a precursor for porcine brain natriuretic peptide

AU Maekawa, Keiji; Sudo, Tetsuji; Furusawa, Mitsuru; Minamino, Naoto; Kangawa, Kenji; Okubo, Hiroaki; Nakanishi, Shigetaka; Matsuo, Hisayuki

CS Daiichi Seiyaku Co. Ltd., Tokyo, 134, Japan

SO Biophysical and Biophysical Research Communications (1983), 157(1), 410-16

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CODEN BBRCA9; ISSN: 0006-291X

LP Journal

LA English

AB Brain natriuretic peptide (BNP) is a new type of natriuretic peptide recently identified in porcine brain. Since the highest concn. of BNP was found in the cardiac atrium, the cDNA library of porcine cardiac atrium was constructed, and the cDNA encoding a BNP precursor was isolated and sequenced. The precursor for porcine BNP (porcine prepro-BNP) is 131 amino acids in length, including a 25 residue putative signal peptide at the N-terminus. Porcine BNP structure is located at the C-terminus of the precursor and is directly followed by a termination codon. Based on structural data recently obtained for γ -BNP (a main storage form of BNP in the heart), prepro-BNP is processed to 106-residue γ -BNP by removal of the signal peptide in the heart, and to low mol. wt. forms, such as BNP-26 and BNP-32, in the brain.

IT 122004-95-5, Deoxyribonucleic acid (pig brain natriuretic factor messenger RNA-complementary). 122006-96-6, Deoxyribonucleic acid (pig clone pBNP34 brain natriuretic factor messenger RNA-complementary).

SL Eif (Properties); BIOI (Biological study)

(nucleotide sequence of)

RN 122006-95-5. CAPLUS

CN DNA (pig brain natriuretic peptide cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggggccccc tgatggcgct tccccggctg ctccctgtcc tggtttttgtca
51 cctgttgctg ttatggatgcc gttcccatcc actgggggtggc gctggccctgg
101 cctcagaact ggcaggata caggagctgc tggaccgcgtt gggagacagg
151 gtctccggcgc tgcajggcgg a cggggacggac ctggagcccccc tccggcagga
201 ccgtggccctc acagaaggctt gggaggcggag ggaagcggcc cccacgggggg
251 ttcttggggcc cggcagtagc atcttccaag tcctccggggg aataacgcggc
301 cccaaacgca tgctgtactc tggctgtttt gggcgaggc tggaccggat
351 cggctccctc agcggccctgg gctgcaatgt gtcaggagg tactga

STN Columbus

RN 122006-96-6 CAPLUS
CN DNA (swine clone pBNP84 brain natriuretic peptide cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggggccccc gnatggcgct tccccgcgtg ctccctgcac tgttcttgca
51 cctgttgcgtg ctaggatgcc gttccatcc actgggtggc gctggcctgg
101 cctcagaact gccaggata caggagctgc tggaccgcct gcgagacagg
151 gtctccgagc tgcaggcga gggacggac ctggagcccc tccggcagga
201 ccgtggcctc acagaagcct gggaggcag ggaagcagcc cccacgggg
251 ttcttggccc ccgcagtagc atcttccaag tcctccgggg aataacgcac
301 cccaaagacga tgcgtgactc tggctgcttt gggcgaggg tggaccggat
351 cggctccctc agcggcctgg gctgcaatgt gctcaggagg tactga

L61 ANSWER 21 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:451444 CAPLUS

DN 111:51444

TI Nucleotide sequence of a cDNA encoding a larval α -globin chain of the amphibian Pleurodeles waltlili

AU Flavin, Michelle; Valentin, Colette; Meunier-Rotival, Michele; Cohen-Solal, Michel

CG Hoppe Henri Mondor, Creteil, 94010, Fr.

SO Nucleic Acids Research (1989), 17(7), 2850

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CJUR: NARHAD; ISSN: 0305-1048

DP Journal

LA English

AB In P. waltlili, Hb undergoes an ontogenetic switch from larval to adult forms. This switch is inducible by thyroid hormones and represents an alternative system to study the regulation of the sequential activation of α -globin genes during erythroid differentiation. A library of erythrocyte cDNAs has been constructed from larvae of P. waltlili at a stage where larval and adult globin genes are expressed simultaneously. The clones corresponding to larval or adult genes were sep'd. by differential screening and identified by hybridization selection and in vitro translation of the selected mRNAs. The sequence of an α -globin cDNA found only at early stages of development is reported.

IT 121630-86-2 Deoxyribonucleic acid (Pleurodeles waltlili)

(α -globin messenger RNA-complementary)

RE PRO (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 121630-86-2 CAPLUS

CN DNA (Pleurodeles waltlili α -globin cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 gttctgtcag ctgaagaagg aggtgaagcc ttggacaggc tgtttgcag
51 cttcgcccaag acgaggacct acttcagccca ctccgaccc tccccggcct
101 ctgtgtacgt gaaacgacat ggaggcaagg tcctaagcgc catcggtgaa
151 gcagccaaac acatcgacag catggaccag gcccgtctta aactgagcga
201 tcgtgcacggc tacaacccctcc gctgtggaccc cgaaaatttc cagctgtgt
251 ctcactgcat tcaggctgtg ctggctgccc acttccctgc cgacttgacc
301 cctcagtgccc aggctgcctg ggacaagtcc ctggccgcag tgtctgcgt
351 cctgacacctcc aagtacatgt aa

STN Columbus

of an addnl. A in the extra arm, has a sequence identical to that of a rabbit liver tRNAPhe. The Alu-like element belongs to the rodent B2 family of short interspersed repetitive nucleotide sequences. This repetitive element, B2Phe, is flanked by 12-bp direct repeats, contains an internal split promoter (block A and block B) for RNA polymerase III and is devoid of an A-rich segment at the 3' end. Like other members of the B2 family, the B2Phe element presents 64% sequence homol. with rat serine tRNA and contains a serine (GCT) anticodon. Both tRNAGAAPhe gene and B2Phe element were found to be transcriptionally active in HeLa cell and Xenopus oocyte nuclear exts. The tRNAPhe gene transcripts were processed during the course of transcription to form mature-size tRNAPhe. The transcription efficiency of the B2Phe element was found to be an order of magnitude higher than that of the tRNAPhe gene. Competition expts. demonstrate that the B2Phe DNA can form a more stable transcription complex than the tRNAPhe gene and compete with it for binding of transcription factors.

IT 121293-42-3 Deoxyribonucleic acid (rat clone prB2Phe B2 element)

RL: PROPE (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 121293-42-3 CAPLUS
CN DNA (rat clone prB2Phe B2 element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ I gggtcttagag agatggctca gcggttaaga gcactggctg ctttccaga
 51 ggtcggtgagt tcaatttcca gaaaccacat gacagctcac aaccataatg
 103 gggttttgtgt ctcagaaacct gagaaggcca ttgtcaagaa gtgagtgaga
 151 aagggtttaaagt taggtggaaat tggccacct ycagagggttc tgtgtacaca
 201 aacgttttattt gtttqtqgac aaggatatcc actgt

168 EASSTIC 2005 62 CAPTION COPYRIGHT 2005 ACS on STN

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AN-1184415643 CAPLUS

2021 RELEASE UNDER E.O. 14176

TI Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire *alpha*-toxin fixation gene cluster of *Klebsiella pneumoniae*

AU Angold, Walter; Rump, Andreas; Klipp, Werner; Priefer, Ursula B.; Puehler, Alfred

CS Fax: 0511 / Univ. Bielefeld, Bielefeld, D-4800/1, Fed. Rep. Ger.

Journal of Molecular Biology (1988), 203(3), 715-38

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D.F. County 1.

The complete nucleotide sequence (24,206 base-pairs) of the *K. pneumoniae* gene region for nitrogen fixation (*nif*) is presented. Coding regions corresponding to the 19 known *nif* genes (including *nifW* and *nifZ*) could be identified. An addnl. open reading frame of 216 base-pairs, called *nifT*, was detected between *nifK* and *nifY*. Search for transcriptional signal structures revealed some unusual features: (1) several possible NifA-binding motifs are present in the intergenic regions between *nifJ* and *nifW* as well as between *nifX* and *nifU*; (2) a perfect NifA-binding motif, preceding the *nifENK* promoter, is located within an inverted repeat structure; (3) structures resembling the consensus *nif* promoter are found within the coding regions of *nifW* and *nifZ* and, together with a NifA-binding motif, in *nifN*. Typical rho-independent termination structures were detected only downstream from the *nifHDKY* and the *nifBQ* operons. Anal. of the deduced amino acid sequences revealed the presence of two Cys-X2-Cys-X2-Cys-X3-Cys-Pro clusters in the pyruvate-flavodoxin

STN Columbus

oxidoreductase NifJ. This arrangement of cysteine residues is normally present only in ferredoxins. A high degree of homol. between the 2 gene products (NifE and NifN) involved in iron-molybdenum cofactor biosynthesis and the 2 nitrogenase component I structural proteins (NifD and NifK) was found. All four proteins are characterized by the conserved motif His-Gly-X2-Gly-Cys, which may play a role in binding the iron-molybdenum cofactor.

IT 120946-05-6, Deoxyribonucleic acid (Klebsiella pneumoniae gene nifW)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 120946-05-6 CAPLUS

CN DNA (Klebsiella pneumoniae gene nifW) (9CI) (CA INDEX NAME)

NTE double stranded

SEQ 1 atgatggagt ggttttatca aattcccgcc gtggacgaac ttgcgtccgc
51 cgaatctttt tttcagttt tcgcgtccc ctatcagccc gagctgcttg
101 gccgctgcag cctgcgggtg ctggcaacgt ttcatcgcaa actccgcgcg
151 gaggtgcgc tgcaaaaccc gtcgaggat aacgaccgcg cgccctggct
201 gctggcgca agactgtctcg cggagagcta tcagcaacag tttcaggaga
251 gcggAACATG a

L61 ANSWER 25 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

AN 120946-05-655 CAPLUS

DN

TA Nucleotide sequence of the nifT, nifY, nifX and nifW genes of K. pneumoniae

AU Lim, William; Cannon, Maura; Buchanan-Wollaston, Vicky; Ally, Abdul; Deshpande, Robert; Dean, Denis; Cannon, Frank

CS Agilent Int. Inc., Cambridge, MA, 02140, USA

SC Lipids and Fatty Acids Research (1988), 16(20), 9860

CDERB, MARHAD; ISSN: 0305-0088

DT 1988-05-20

LR 1988-05-20

AB Nucleotide sequences of the nifT, nifY, nifX, and nifW from Klebsiella pneumoniae were determined. These genes are within operons in the nif cluster.

IT 120946-05-6, Deoxyribonucleic acid (Klebsiella pneumoniae gene nifW)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 120946-05-6 CAPLUS

CN DNA (Klebsiella pneumoniae gene nifW) (9CI) (CA INDEX NAME)

NTE double stranded

SEQ 1 atgatggagt ggttttatca aattcccgcc gtggacgaac ttgcgtccgc
51 cgaatctttt tttcagttt tcgcgtccc ctatcagccc gagctgcttg
101 gccgctgcag cctgcgggtg ctggcaacgt ttcatcgcaa actccgcgcg
151 gaggtgcgc tgcaaaaccc gtcgaggat aacgaccgcg cgccctggct
201 gctggcgca agactgtctcg cggagagcta tcagcaacag tttcaggaga
251 gcggAACATG a

L61 ANSWER 26 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

STN Columbus

Full Text

AM 1989:151808 CAPLUS
DN 110:151808

TI Expression of a fibrinogen fusion peptide in Escherichia coli: a model thrombin substrate for structure/function analysis

AJ Lord, Susan T.; Fowlkes, Dana M.

CS Med. Sch., Univ. North Carolina, Chapel Hill, NC, 27599-7525, USA

SO Blood (1989), 73(1), 166-71

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CODEN: BLOOAW; ISSN: 0006-4971

DT Journal

LA English

AB A vector was constructed which expressed a tripartite protein (tribrid) consisting of amino acids 1-50 of the fibrinogen α chain followed by 60 amino acids of chicken collagen and the β -galactosidase protein from E. coli. Cell lysates run on SDS-polyacrylamide gels contained the predicted band of mol. wt. 125,000. The tribrid reacted with a monoclonal antibody, Mab-Y18, which recognizes the N-terminus of the α chain. When cell lysates were incubated with thrombin, fibrinopeptide A was released. By including 1 heterogeneous oligonucleotide in the construction, plasmids were generated that encoded 3 specific amino acid substitutions. Surprisingly changing glycine-14 to valine did not alter thrombin cleavage, although recognition by Mab-Y18 was lost. Substitution of isoleucine for arginine-23 did not alter either thrombin cleavage or monoclonal recognition. Substitution of leucine for arginine-16 altered thrombin cleavage; unexpectedly, recognition by Mab-Y15 was not changed.

PT 035798-32-5P

AB: CPN (Synthetic preparation); PREP (Preparation)

(prepn. of)

RN 135798-32-5 CAPLUS

CN DNA: (A-A-C-T-A-C-A-A-T-G-C-C-C-T-T-C-T-G-G-C-T-G-C-A-G-G) (9CI) (CA INDEX NAME)

SPR single stranded

SEQ: tactacaat gccttcgg ctgcagg

LCI ANSWER 27 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AM 1988:52100 CAPLUS

DN 110:52100

TI The cDNA and derived amino acid sequences for human and bovine matrix Gla protein

AJ Kieret, Michael C.; Bauer, Diane M.; Young, Daru; Wermser, Kathleen M.; Aguirre, Frank R.; Barr, Phillip J.

CS Chiron Corp., Emeryville, CA, 94608, USA

CO Peptides Research (1988), 16(11), 5213

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The cDNAs for matrix Gla protein (MGP) of human and cattle bone were isolated and sequenced. The amino acid sequences of the precursor proteins encoded by the cDNAs were 84.5% homologous, and the human cDNA-coded precursor was 91.6% homol. to that of rat MGP precursor. Unlike previously detd. vitamin K-dependent protein structures, the MGPs from human and rat do not contain a propeptide that is cleaved at a basic-K-basic-basic amino acid processing motif within the substrate recognition sites for vitamin K-dependent glutamic acid γ -carboxylase.

STN Columbus

IT 118441-10-4, Deoxyribonucleic acid (ox protein MGP messenger

RNA-complementary)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 118441-10-4 CAPLUS

CN DNA (cattle protein MGP cDNA) (9CI) (CA INDEX NAME)

NTS: doublestranded

SEQ 1 atgaagagcc tgctccttct ctccatcctg gctgccttgg ccgtggcagc
51 tctgtgttat gaatctacg aaagcctgga atcctatgaa atcaatccct
101 tcattaacag gagaaacgct aacagctta tatcaccaca acagagatgg
151 agagcaaaag cccaagagag atatcgagaa ctcaacaagc ctcaatacga
201 gctcaaccgg gaagttgtg atgacttcaa actttgcga cgctatgcca
251 tggtgtatgg atacaatgct gcctacgacc gttattccg gcagcgccga
301 gggggccaaat ga

L61 ANSWER 28 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1069:51984 CAPLUS

DN 110:51984

TI Colicin E3, a DNase which indicates an evolutionary relationship between colicins E2 and E3

AU Toba, Kuni; Masaki, Haruhiko; Ohta, Takahisa

CS Dep. Agric. Chem., Univ. Tokyo, Tokyo, 113, Japan

SE Jpn Jik of Bacteriology (1988), 170(7), 3237-42

CODE: SOBRAY; ISSN: 0621-9193

Source:

Publ.:

AB Colicin E3-J and its immunity protein were characterized with regard to their activities and gene structures. Colicin E3 is a complex of protein A and B. Protein A (the naked E3) exhibits an apparently nonspecific DNase activity that is inhibited by protein B (the immunity protein), as in the case of colicin E2. The nucleotide sequence of the downstream half of the colicin operon of ColE3-J was detd. to be highly homologous to that of ColE2-P9, with the exception of the hot spot region of the 3'-terminal segment of the colicin gene and the adjacent immunity gene. The immunity-like gene of ColE3-CA38 was, as assumed previously, extensively homologous to the immE8 gene of ColE8-J, and thus, ColE8-J was shown to be situated between ColE2-P9 and ColE3-CA38 in the evolution of the E-group Col plasmids.

IT 113280-05-6, Deoxyribonucleic acid (plasmid ColE8-J colicin E 8

lysis peptide gene lys)

RL: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of).

RN 113280-05-6 CAPLUS

CN DNA (plasmid ColE8-J colicin E 8 lysis peptide gene lys) (9CI) (CA INDEX NAME)

NTS: doublestranded

SEQ 1 atgaaaaaaaaa tggcagggtt tattttattt cttcttgcat tcattttttct
51 ggctgcattgt tggccaaactt atatccggaa tggccagggtt gggaccgtat
101 gccccgttcatc aacagctgaa gtgaccggat tagcaacgca gtaa

L61 ANSWER 29 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

STN Columbus

AN 1988:623655 CAPLUS
DN 109:223655
TI Nucleotide sequence and gene organization of sea urchin mitochondrial DNA
AU Jacobs, Howard T.; Elliott, David J.; Math, Veerabhadracharya B.;
Farquharson, Andrew
CS Dep. Genet., Univ. Glasgow, Glasgow, G12 8QQ, UK
SO Journal of Molecular Biology (1988), 202(2), 185-217
=====

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal
LA English

AB The 15,650 base-pair mitochondrial genome of the sea urchin *Strongylocentrotus purpuratus* has been cloned and sequenced. It exhibits a novel organization that suggests the primary of post-transcriptional gene regulation. The same 13 polypeptides, 2 rRNAs and 22 tRNAs are encoded as in other animal mitochondrial DNAs, but are organized with extreme economy: non-coding information between genes is almost completely absent, some stop codons are generated post-transcriptionally and tRNA sequences are interspersed between only a minority of other structural genes. The genome uses a variant genetic code, in which AAA specifies asparagine, ATA isoleucine, TGA tryptophan, and AGN serine, and has an unusual pattern of codon bias. The order of genes show several differences from that of vertebrates. The genes for the large (16 S) rRNA and for NADH dehydrogenase subunit 4L (ND4L) are in different positions, located resp. between those encoding ND2 and cytochrome oxidase subunit I (COI) and between COI and COII. This organization is conserved amongst at least 4 regular echinoids diverging by some 225 million years. Most tRNA genes are also in different positions. The only long unassigned sequence in the genome (121 base-pairs) is located within a cluster of 15 tRNA genes. It contains elements resembling some of those found in the displacement (D) loop of vertebrate mtDNAs, notable polyuridine and polyadenylidine tracts that may play a role in regulating transcription and the initiation of replication. The sepn. of the rRNA genes from each other and from the putative control region imposes special demands on the arrangement of the genome.

IR 1988046-2
PR: PROPERTIES; BIOLOGY (Biological study)
RN: Nucleotide sequence of

RG 1988048-5 CAPLUS
CN DNA (*Strongylocentrotus purpuratus* clone .lambda.mt1 reduced nicotinamide adenine dinucleotide dehydrogenase subunit 3 gene) (9CI) (CA INDEX NAME)

NB: double stranded

SEQ:
1 atgacaacta taatctttttt gtttagtata accattgcag tagccgtagt
51 gcttgqactg gcttcgtatg ccctgcctaa acgcaccagg gatagagaaa
101 aagactccccc ttacggatgt ggctttgate cgcttaaatc cggccgatta
151 ctttttcat tccgggtttt tcttgtcgcc attttgggg tgcgttttga
201 cctagaataa gcaatgtatc ttatcttacc agctgttgg ctgtataactc
251 ccctcccac tttaattcca attcataatgg tttttatgg tatcttgaca
301 ctccgattag ttttcgatgt mataaaagg ggcttagaat gagcagatgt
351 a

L61 ANSWER 30 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:505710 CAPLUS

DN 109:105710

TI Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome c

STN Columbus

oxidase
AU Zeviari, Massimo; Sakoda, Saburo; Sherbany, Ariel A.; Nakase, Hirofumi;
Rizzuto, Rosario; Samitt, Craig E.; DiMauro, Salvatore; Schon, Eric A.
CS Coll. Physicians Surg., Columbia Univ., New York, NY, 10032, USA
SO Gene (1988), 65(1), 1-11

=====
CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB The authors isolated a full-length human fetal muscle cDNA clone specifying the nuclear-encoded subunit Vb of the human mitochondrial respiratory chain enzyme, cytochrome c oxidase (COX; EC 1.9.3.1), and a partial-length cDNA clone from brain specifying the analogous bovine subunit. The 2 cDNAs are 85% identical at the nucleotide level. Similar to other proteins imported into mitochondria, the deduced human COX Vb protein contains a presequence, 31 amino acids long, rich in basic residues. There was no evidence for tissue-specific transcripts for subunit Vb of human COX, as Northern anal. of total RNA for human muscle, liver, and brain showed a single, identically sized transcript in each cell type, whereas partial-length cDNA clones isolated from human muscle and endothelial cell cDNA libraries were identical in sequence to the fetal muscle cDNA.

IT 116243-65-3, Deoxyribonucleic acid (human clone HCOX5.21

cytochrome oxidase subunit Vb mRNA-complementary)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 116243-65-3, CAPLUS

CM DNA (human clone HCOX5.21 cytochrome oxidase subunit Vb cDNA) (9CI) (CA
IUPAC/VAE)

NT: doublestranded

SEQ:
1 tagctcaa ggttaacttcg cggagctgga acgctggccg cgcaaggccc
2 gggtgcgg ggcggccatgtt cggcgccgc gatgcgtcc atggcatctg
3 gaggtgggtt tccactgtat gaagagcagg cgtactgggtt ggagagggag
4 ttatgttgtt ctgaaagaa agggactggac ccatacatg tactggcccc
5 aaaggagct ccaggcacca gggagaccc taatttagtc ccctccatct
6 caacaagag gatagttagtc gcatctgtg aagaggacaa taccagcgtc
7 gtctggttt ggctggacaa agggcaggcc cagcgatgcc cccgctgtgg
8 ccgtccattac aagctggtgc ccccgacactg ggcacactga

LEN: ANSWER 31 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987-667910 CAPLUS

DN 100-667910

TI Human cysteine-proteinase inhibitors: nucleotide sequence analysis of three members of the cystatin gene family

AU Gaitan, Eiichi; Kim, Hyung Suk; Smithies, Oliver; Maeda, Nobuyo

CS Lab. Gen., Univ. Wisconsin-Madison, Madison, WI, 53706, USA

SO Gene (1987), 61(3), 329-38

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CODEN: GENED6; ISSN: 0378-1119

DT Original

LA English

AB Three genes from the human cystatin gene family of cysteine-proteinase inhibitors were isolated from a phage λ library contg. HindIII digests of human genomic DNA. Two of the genes code for salivary cystatin CN and SA; the third is a pseudogene. The cloned genes were identified with a probe made from a salivary cystatin cDNA. The complete nucleotide

STN Columbus

sequence of the gene that codes for the precursor form of the neutral salivary protein, cystatin SN, was detd. The gene, which was named CST1, contains 3 exons and 2 intervening sequences. The expected CAT and ATA boxes are present in the 5'-flanking region of the gene. Partial nucleotide sequence detn. of a second gene revealed that it codes for the precursor form of the acidic salivary protein, cystatin SA. This gene, designated CST2, has the same gene organization as CST1. The complete nucleotide sequence of a 3rd gene was detd. It does not contain a typical ATA box, and in addn., a premature stop codon and a frameshift deletion mutation occur within the gene. These inactivation mutations show that this gene, designated CSTP1, is a cystatin pseudogene. These data combined with genomic Southern-blot analyses show that the cystatin genes form a multigene family with ≥7 members.

IT 115682-20-7, Decoxyribonucleic acid (human clone CSTP1 pseudogene

CSTP1)

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 115682-20-7 CAPLUS

CN DNA (human clone CSTP1 pseudogene CSTP1) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgccccttc acttccctgc acttccccct ttcactcttt tggccttgct
51 ccagcagacc acaacctggc ccctgcacac tccactgccc ttgctggctg
100 ccctgttgtt ggccttagcc tag

L61 ANSWER 38 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986-217075 CAPLUS

DN 100..11175

TI Human lysozyme and its manufacture and secretion with Saccharomyces

IN Ueda, Yoshifumi; Muraki, Michiro; Harada, Nobuhiko; Tanaka, Hideaki; Matsunaga, Satoshi

PA Agency of Industrial Sciences and Technology, Japan

SO Jpn Kokai Tokkyo Koho, 15 pp.

COPYR: JKXXAF

DT Patent

LA Japanese

FAN.CN 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|----|-------------|------|----------|-----------------|----------|
| PT | JP 08140482 | A2 | 19871029 | JP 1985-268218 | 19851128 |
| PT | JP 08140474 | A4 | 19911107 | | |
| PT | JP 08140479 | A2 | 19910803 | JP 1990-332827 | 19901129 |
| PT | JP 08140916 | A4 | 19930903 | | |

PRAV: JP 1985-268218

AB Human lysozyme (I) precursor composed of I and chicken I signal peptide is manufactured and secreted by *Saccharomyces*. The DNA sequence encoding I precursor, which sequence is composed of a synthetic DNA fragment coding for the signal peptide of chicken I and the structural gene coding for human I (isolated from pHLY-1), was cloned into pHLYSIG. The SalI-HindIII fragment (800 basepair) of pHLYSIG contg. the fused sequence was subcloned into YEp51 contg. the GAL10 promoter to form the expression plasmid YEp-pHLYSIG. *S. cerevisiae* KK4 (YEp-pHLYSIG) cultivated by a conventional method secreted 60% of the I precursor into the medium (at stationary phase). The purified I precursor possessed bacteriolytic activity comparable to the com. I.

IT 115683-29-4

RL: PRP (Properties)

STN Columbus

(expression in *Saccharomyces cerevisiae* and nucleotide sequence of)

RN 114880-29-4 CAPLUS
CN DNA, d(A-T-G-A-G-G-T-C-T-T-G-C-T-A-A-T-C-T-T-G-G-T-G-C-T-T-G-C-T-C-C-T-G-C-C-C-T-G-G-C-T-C-T-G-G-G-G), complex with DNA
d(C-C-C-C-A-G-A-G-C-A-G-C-C-A-G-G-G-G-C-A-G-G-A-A-G-C-A-A-A-G-C-A-C-C-A-A-G-A-T-T-A-G-C-A-A-A-G-A-C-C-T-C-A-T) (1:1) (9CI) (CA INDEX NAME)

SEQ 1 atgaggcttt tgatatatctt ggtgtttgc ttccctggccc tggctgtct
51 ggggg

L61 ANSWER 33 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1988:107263 CAPLUS

DN 108:107263

TI Cloning and characterization of a novel T cell activation gene
AU Burd, Parris R.; Freeman, Gordon J.; Wilson, Stephen D.; Berman, Michael;

DeKruyff, Rosemarie; Billings, Paul R.; Dorf, Martin E.

CS Dana-Farber Cancer Inst., Harvard Med. Sch., Boston, MA, 02115, USA

SO Journal of Immunology (1987), 139(9), 3126-31

====

CODEN: JOIMA3; ISSN: 0022-1767

DT Journal

LA English

AB The technique of subtractive hybridization was used to identify a T cell gene selectively expressed during activation via the antigen-receptor pathway. This gene, termed TCA3 (for T cell activation), encodes a mRNA which is expressed following concanavalin A (Con A) activation of T cell clones at levels of approx. 1% total poly(A)-contg. mRNA. The cDNA isolate, termed TCA3.0, is 512 bases in length, excluding poly(A), and encodes a predicted 93-amino acid protein having the characteristics of a secreted polypeptide of approx. 69 amino acids. The genomic organization of TCA3 was detd. for two λ phage clones and was found to be a single copy gene contg. at least three exons dispersed over less than 4.7 kb. The temporal appearance of TCA3 mRNA in response to several activating agents was examd. It is not transcribed in response to interleukin 2 stimulation, but is transcribed in response to either antigen or Con A stimulation and can be detected as early as 1 h poststimulation. Expression of TCA3 in response to Con A is blocked by cyclosporin A treatment. The combined data suggest that TCA3 may represent a new lymphokine.

IT 113314-69-5

RL: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)

RN 113314-69-5 CAPLUS

CN DNA (mouse clone TCA3.0 gene TCA3 glycoprotein cDNA) (9CI) (CA INDEX NAME)

SEQ 1 atgaaaccca ctgccatggc actgatgtgc ctgctgtgg ctggcggtgt
51 gatacaggat gttgacagca agagcatgtct acgggttc aatagctgt
101 gcttgaacac cttgaagaaa gagctcccc tgaaggttat ccagtgttac
151 agaaagatgg gctccctctg tccgtatccc ccagctgtgg tattcaggct
201 qaacaatggt agagaaagct ggcgccteaa taacaaaacg tgggttcaaa
251 atcacatgaa gaaggtgaat ccctgtctaa

STN Columbus

AB The primary structures of the immunity (Imm) and lysis (Lys) proteins, and the C-terminal 205 amino acid residues of colicin E8 were deduced from nucleotide sequencing of the 1265-bp *Cla*I-*Pvu*I DNA fragment of plasmid ColE8-J. The gene order is col-imm-lys confirming previous genetic data. A comparison of the colicin E8 peptide sequence with the available colicin E2-P9 sequence shows an identical receptor-binding domain but 20 amino acid replacements and a clustering of synonymous codon usage in the nuclease-active region. Sequence homol. of the 2 colicins indicates that they are descended from a common ancestral gene and that colicin E8, like colicin E2, may also function as a DNA endonuclease. The native ColE8 imm (resident copy) is 258-bp long and is predicted to encode an acidic protein of 9604 mol. wt. The 6 amino acid replacements between the resident imm and the previously reported non-resident copy of the ColE8 imm ([E8 imm]) found in the RNase-producing ColE3-CA38 plasmid offer an explanation for the incomplete protection conferred by [E8 Imm] to exogenously added colicin E8. Except for 1 nucleotide and amino acid change in the putative signal peptide sequence, the ColE8 lys structure is identical to that present in ColE2-P9 and ColE3-CA38.

IT 113256-05-6

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 113256-05-6 CAPLUS

CN DNA (plasmid ColE8-J colicin E 8 lysis peptide gene lys) (9CI) (CA INDEX NAME)

NTE doublestranded

SEN 1. aaaaaaaaaaa taacatggat tattttatgt ctttttgcat tcacttattt
2. tggttgtcatgt caggcaaact atatccggga tgttcagggc gggaccgtat
3. 01 aacgtcatac aacagctya gtgaecggat tagcaacgcgtaaa

REF ID: A8397P 26 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

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AN 1988-52779 CAPLUS

DM 136-38724

11 Molecular cloning of matrix Gla protein: implications for substrate
recognition by the vitamin K-dependent γ -carboxylase

AU *Fraser, Paul A.; Fraser, James D.; Metz-Virca, Gabrielle*

CC Rep. Prof., Univ. California, San Diego, La Jolla, CA, 92093, USA

60 Proceedings of the National Academy of Sciences of the United States of America (1987), 84(23), 8335-9.

COLONY: PNASA6; ISSN: 0027-8424

DT Sonstige

LA English

AB watrix-Gla protein (MGP), a low mol. wt. protein found in bone, dentin, and cartilage, contains 5 residues of the vitamin K-dependent amino acid γ -carboxyglutamic acid (Gla). Antibodies raised against MGP and oligonucleotide probes were used to screen a λ gt11 cDNA library constructed from the rat osteosarcoma cells (line ROS 17/2) that had been pretreated with 1 α ,25-dihydroxyvitamin D3. By sequencing several cloned cDNAs, a 523-base-pair sequence that predicts an 84-residue mature MGP and a 19-residue hydrophobic signal peptide was established. The 84-residue mature rat MGP predicted from the cDNA sequence has an addnl. 5 residues at its C terminus (-Arg-Arg-Gly-Ala-Lys) not seen in the sequence of MGP isolated from bovine bone. The structure of rat MGP provides insight into the mechanisms by which the vitamin K-dependent γ -carboxylase recognizes substrate. The present studies show that MGP, unlike other vitamin K-dependent proteins, lacks a propeptide. The

STN Columbus

absence of an MGP propeptide demonstrates that γ -carboxylation and secretion of vitamin K-dependent proteins need not be linked to the presence of a propeptide or to its proteolytic removal. The propeptides of other vitamin K-dependent proteins are structurally homologous, and there is evidence that this homologous propeptide domain is important to substrate recognition by the γ -carboxylase. Mature MCP has a sequence segment (residues 15-30) that is homologous to the propeptide of other vitamin K-dependent proteins and probably serves the same role in γ -carboxylase recognition. Rat MGP also has a second sequence that has recently been identified in all known vitamin K-dependent vertebrate proteins, the invariant unit Glu-Xaa-Xaa-Xaa-Glu-Xaa-Cys (EXXXEXC). Since the glutamic residues in this unit are sites of γ -carboxylation, it has been suggested that the EXXXEXC unit could allow the γ -carboxylase to discriminate between substrate and product. The demonstration that 2 structures common to vitamin K-dependent proteins, the homologous propeptide domain and the invariant EXXXEXC unit, are in mature MGP indicates that des- γ -carboxy-MGP should be an excellent in vitro γ -carboxylase substrate for anal. of mechanisms involved in substrate recognition and product dissociation.

IT 113014-36-1

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)
RN 113014-36-1 CAPLUS
CN DNA (rat clone λ MGP-6/ λ MGP-1 protein MGP cDNA) (9CI) (CA
INDEX NAME)

NTE doublestranded

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STN Columbus

CN DNA (Escherichia coli gene HU-2) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaacaaga ctcaactgat tgatgttaatt gcagagaaaag cagaactgtc
51 caaaaaccgg gctaaagctg ctctggagtc cactctggct gcaattactg
101 agtctctgaa agaaggcgat gctgtacaac tggttgggtt cggtaccc
151 aaagtgaacc accgcgctga gcgtactggc cgcaacccyc agaccggtaa
201 agaaaatcaaatttgcgcag ctaacgtacc ggcattttt tctggcaagg
251 cactgaaaga cgcaatgtt aaa

L61 ANSWER 38 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1987:612642 CAPLUS

DN 107:212642

TI Cloning, DNA sequence, and expression of the Rhodobacter sphaeroides light-harvesting B800-850- α and B800-850- β genes

AU Kiley, Patricia J.; Kaplan, Samuel

CS Dep. Microbiol., Univ. Illinois, Urbana, IL, 61801, USA

SO Journal of Bacteriology (1987), 169(7), 3268-75

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB Two decynoligonucleotide probes were synthesized in accordance with the available amino acid sequence of the B800-850- β polypeptide from R. sphaeroides, and were used to isolate a 2.6-kilobase PstI fragment from R. sphaeroides 2.4.1 chromosomal DNA. Identification of the B800-850- β and B800-850- α structural genes, pucB and pucA, was confirmed by DNA sequencing. Northern (RNA) blot anal., using restriction endonuclease fragments from the cloned genes as probes, revealed a single 2.6-kilobase-specific, highly stable transcript of approx. 640 bases present in photosynthetically grown cells. In vitro transcription-translation anal. of the puc operon revealed that the max. synthesis of the puc operon gene products was achieved when the entire 2.6-kilobase PstI fragment was used as the template, although a 537-base-pair XmaIII fragment was sufficient to direct the synthesis of pucB and a pucA fusion product.

TT PROPERTIES

RL (Properties); BIOL (Biological study)

NUCLEOTIDE SEQUENCE OF

RN 107:70-51-6 CAPLUS

CN DNA (Rhodobacter sphaeroides strain NCIB 8253 clone pMA81 gene pucA) (9CI) (CA INDEX NAME)

NTE Doublestranded

SEQ 1 atgaccaacg gcaaaaatcg gtcgtggtg aaaccgaccg tcggcggtcc
51 gttgttccctc agegcgtggcg tcatcgccctc cgtcgttatac caccgtgtct
101 tgcgtgacgac caccacctgg ctggccgcct actaccaagg ctcggctgcg
151 ctccggcccg agtaa

L61 ANSWER 39 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1987:592060 CAPLUS

DN 107:192060

TI Observations on the structure of two human 7SK pseudogenes and on

STN Columbus

homologous transcripts in vertebrate species
AU Humphries, Peter; Russell, S. E. Hilary; McWilliam, Peter; McQuaid,
Shirley; Pearson, Colin; Humphries, Marian M.
CS Dep. Genet., Trinity Coll., Dublin, Ire.
SO Biochemical Journal (1987), 245(1), 281-4
====

CODEN: BIJOAK; ISSN: 0306-3275

DT Journal

LA English

AB A comparison of the sequence of 2 human 7SK RNA pseudogenes, covering approx. 190 and 240 base-pairs of the structural gene, is presented. Both repeated elements are flanked by direct repeats and begin at the 5' end of the gene. Each terminates approx. 90 base-pairs short of the 3' end, the latter representing a contiguous sequence and the former carrying an internal deletion of ~40 base-pairs, this region being flanked in the progenitor gene by short repeated sequences. Southern blotting using a human 7SK pseudogene probe illuminated a series of multiple restriction fragments in mammalian genomes, with generally fewer fragments in the genomes of birds and reptiles and a single reactive fragment in DNA from terrapin (*Pseudemys scripta elegans*) and *Xenopus laevis* (South African clawed toad). In the latter case, this fragment was only detectable on long exposure under the hybridization stringencies employed. 7SK transcripts were readily detectable in all mammalian, avian, reptilian, and amphibian species analyzed, although the gene appeared to be expressed at rather low levels in the ovaries of *Xenopus laevis*, possibly accounting for its failure to have become dispersed via retroposition in this species.

IT 110341-3-0

RE: RSP (Properties); BYCL (Biological study)
(nucleotide sequence of)

RN 110341-23-0 CAPLUS

CA RNA, human:RNA 7-3 pseudogene A) (9CI) (CA INDEX NAME)

NFT Gene not found

SEQ 1 aatcgaggcc aatctggctg cgacatctgt cccactgtat taccagggtt
2 gatccgcgtg atctgtctgg cttaggcgggt ctctcttttc tccttcagcc
131 ctccatgtgt gtacctcctg aagcggactg gtcttcagtc aagggttagac
151 gagtagctgt gctccccctgc tagaacctcc aaacaagtc tcaagaagga
201 ggtatttag

BSI MODEM 10 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

BN 110341-23-0 CAPLUS

DN J071139762

TI Structural and functional analysis of a human 7 SK RNA gene

AU Kriegler, Winfried; Benecke, Bernd Joachim

CS Dep. Biochem., Ruhr-Univ., Bochum, D-463/1, Fed. Rep. Ger.

SO Journal of Molecular Biology (1987), 195(1), 31-41
====

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

AB Using purified RNA from HeLa cells, a cDNA encoding an almost entire 7 SK RNA was cloned and sequenced. This cDNA probe was used to isolate 7 SK RNA gene sequences from a human genomic library by high-stringency colony hybridization. In order to differentiate between functional genes and related sequences, a rapid in vitro transcription assay of purified phage DNA was used. With this addnl. screening criterion applied to selected

STN Columbus

clones, one recombinant phage was obtained that contained a complete 7 S K RNA gene and, immediately adjacent to its 3' end, a truncated pseudogene. The nucleotide sequence of both genes including the flanking regions has been detd. The functional integrity of the isolated 7 S K RNA gene was verified by in vitro transcription studies with cell-free exts. and by fingerprinting of the specific transcripts with RNase T1. Under optimal ionic conditions, the transcription efficiency in vitro of this 7 S K RNA gene was found to be comparable to that of a human 7 S L RNA gene. A series of 5'-deletion mutants showed that transcription of 7 S K RNA in vitro depends on 5'-flanking sequences. The region up to position -67 was detd. to be essential for efficient transcription in vitro of 7 S K RNA. While apparently a variety of 7 S K related sequences is distributed within the human genome, hybridization of 5'-flanking sequences to genomic DNA revealed that possibly not more than one copy of this gene is present per haploid genome.

IT 110735-47-3

RL: FRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

BN 110735-47-2 CAPLUS

CN DNA (Human clone p9.1 7-3 RNA gene) (9CI) (CA INDEX NAME)

NTE: doublestranded

SE(2) 1' ggatgtgagg cgatctggctt ycgacatctg tcacccattt gatcgccagg
51' gtggattcgg ctgtatctggc tggcttaggcg ggtgtccccctt tcctccctca
101' atgcgtccatgt tgccgtccctc csgaagctgc gcgcgtcggtc gaagaggacg
151' accatcccccg atagaaggagg aaccggttttc ggtcaagggtt atacgagtag
201' atgcgtcccccc ctgtcttggaaat cccaaaacaa gctctcaagg tccatttgta
251' tggatgtcgta gggtagtcctt ycttccaaga ctgcagacac atccaaatgt
301' atgcgttcgtat gtggccatgtt gatctttttt t

L-50 INDEX-P 14 OF 52 CAPLUS : COPYRIGHT 2005 ACS on STN

卷之三

AN 1577.56-1924 CAPLUS

E.I. - 10014368624

AT Cloning and oxygen regulated expression of genes coding for the reaction center and light harvesting polypeptides of *Rhodopseudomonas sphaeroides*

AJ. ASHBY, Mark K.; Coomber, Shirley A.; Hunter, C. Neil

CS Dep. Pure Appl. Biol., Imp. Coll. Sci. Technol., London, SW7 2BB, UK

SC Progr. Photosynth. Res., Proc. Int. Congr. Photosynth., 7th (1987),

Meeting Date 1986, Volume 4, #33-6. Editor(s): Biggins, John. Publisher: Nijhoff, Dordrecht, Neth.

COLDEN'S SUGARAT

Confidence

LA ENGLISH

卷之三

complexes: B800-850, B875, and the reaction center. Cloned gene probes were used to study the levels of transcripts for these proteins in cells induced to pigment. The genes for the reaction center and B875 are co-regulated, with a peak of transcription at 50-90 min after induction. The B875 apoprotein gene is encoded on 2 transcripts, 2.6 and 0.5 kb; the 2.6 kb. message also encodes the reaction center. The nucleotide sequence of the B800-850 genes was detd. The B600-350 genes are transcribed on one 0.5 kb transcript; the level of mRNA does not reach a peak until 6 h after pigment induction.

IT 109370-~~1~~-6

RL: EPP (Properties); BIOL (Biological study)
(nucleotide sequence of)

STN Columbus

RN 109370-51-6 CAPLUS
CN DNA (Rhodobacter sphaeroides strain NCIB 8253 clone pMA81 gene pucA) (9CI)
(CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaccaacg gcaaaaatctg gtcgtgggtg aaaccgaccg tcggcggttcc
51 gctgtttcctc agcgtgcgg tcatcgccctc cgtcgttatac caccgtgtgc
101 tgctgacgac caccacctgg ctgcccgcct actaccaagg ctccggctgcg
151 gtcgcggccg agtaa

L61 ANSWER 42 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:453079 CAPLUS

DN 107:53079

TI Cloning, nucleotide sequence, and transfer of genes for the B800-850 light harvesting complex of Rhodobacter sphaeroides

AU Ashby, Mark K.; Coomber, Shirley A.; Hunter, C. Neil

CS Dep. Pure Appl. Biol., Imp. Coll., London, SW7 2BB, UK

SO FEBS Letters (1987), 213(2), 245-8

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CODEN: FEBLAS; ISSN: 0014-5793

DT Journal

LA English

AB Two genes that encode the α and β polypeptides of the major light-harvesting complex of *R. sphaeroides*, B800-850, were cloned and sequenced through the use of oligonucleotides based upon the known polypeptide sequences. These genes, pucA and B, are transcribed in the same direction, B, A, are of 150 and 164 nucleotides resp., and are sepd. by a unique region of 14 nucleotides. Transfer of these genes to mutant M21 lacking the B800-850 complex has been accomplished, and absorbance spectra of recombinant strains M2131 and M2184 show that expression of pucA and B is comparable to levels found in the wild type.

IP 109370-51-6

SPR (Properties); BIOC (Biological study)

NU (Nucleotide sequence of) A17

RN 109370-51-6 CAPLUS

CN DNA (Rhodobacter sphaeroides strain NCIB 8253 clone pMA81 gene pucA) (9CI)
(CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaccaacg gcaaaaatctg gtcgtgggtg aaaccgaccg tcggcggttcc
51 gctgtttcctc agcgtgcgg tcatcgccctc cgtcgttatac caccgtgtgc
101 tgctgacgac caccacctgg ctgcccgcct actaccaagg ctccggctgcg
151 gtcgcggccg agtaa

L61 ANSWER 43 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:114518 CAPLUS

DN 109:114518

AB cDNA sequences of two apolipoproteins from lamprey

AU Pontes, M.; Xu, X.; Graham, D.; Riley, M.; Doolittle, R. F.

CS Dep. Chem., Univ. California, San Diego, La Jolla, CA, 92093, USA

SO Biochemistry (1987), 26(6), 1611-17

====

STN Columbus

CODEN: BICHAW; ISSN: 0066-2960

DT Journal

LA English

AB The messages for two small, but abundant, apolipoproteins found in lamprey blood plasma were cloned with the aid of oligonucleotide probes based on amino-terminal sequences. In both cases, numerous clones were identified in a lamprey liver cDNA library, consistent with the great abundance of these proteins in lamprey blood. One of the cDNAs (LaL1) has a coding region of 105 amino acids that corresponds to a 21-residue signal peptide, a putative 8-residue propeptide, and the 76-residue mature protein found in blood. The other cDNA (LaL2) codes for a total of 191 residues, the first 23 of which constitute a signal peptide. The two proteins, which occur in the high-d. lipoprotein fraction of ultracentrifuged plasma, have amino acid compns. similar to those of apolipoproteins found in mammalian blood; computer anal. indicates that the sequences are largely helix-permissive. When the sequences were searched against an amino acid sequence data base, rat apolipoprotein IV was the best matching candidate in both cases. Although a reasonable alignment can be made with that sequence and LaL1, definitive assignment of the 2 lamprey proteins to typical mammalian classes was not made.

IT 106946-82-1

RE: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106946-82-1 CAPLUS

CN DNA (*Petromyzon marinus* clone LaL1 lipoprotein cDNA) (9CI) (CA INDEX NAME)

NTC doublestranded

SEQ 1. tttgtaaagctcc acgtggctgc cctggcact ctgcgcgtcg tctgcacatcc
2. ggttgcaggg tccgagggccg cgccccaaaggc gatgtccgac ccggccgtgg
3. tcaaggccca gctttccccc gacgccttc gggagagctt caagaatgtg
4. tccatgtggat tcgttggat ggtgcacggc ctgcagaccc ccaacatcg
5. ggatggacgccc aatggccctgtt acaccgacac ggtggccgtg ctgaccggcg
6. aatgtccagaa gatccggcggat aacgtcacca agatgtacca ggtgtacgtg
7. qaggtccaaaggc agcacttag

EDT ANSWER 44 OF 62 CAPLUS. COPYRIGHT 2005 ACS ON STN

SID TaxID

AN 106946-82-1 CAPLUS

DN 106946-82-1

AB A sequence upstream from the coding region is required for the transcription of the 7SK RNA genes.

AU Murphy, Shona; Tripodi, Ma.; Melialuisa

CS Solari Res. Cent., Siena, Italy

SO Nucleic Acids Research (1986), 14(23), 9243-60

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CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB Two recombinant λ phages were isolated and characterized that contain sequences homologous to 7SK RNA and code for a RNA 330 nucleotides long when in vitro transcription system. S1 mapping of the transcript shows that this RNA corresponds to the 7SK RNA obtained from human cells, indicating that the two recombinant phages contain genes coding for 7SK RNA. The transcription of these genes is polymerase III dependent. Sequences upstream from the start of transcription are essential for in vitro synthesis of 7SK RNA, suggesting that internal promoter elements, if present, are not sufficient to support the synthesis of 7SK RNA. A region

STN Columbus

of homol. with the upstream sequences of the genes for U6 RNA, 7SL RNA, and *Bombyx mori* alanine tRNA is found within 50 base pairs from the transcription start point. Within the homologous region a motif common to the four genes is a TATA-like box, placed at position -30 to -25 of the 7SK RNA gene, which is typical of the polymerase II promoter region.

IT 106907-89-5

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106907-89-5 CAPLUS

CN DNA (human clone 7SK33 7-3 RNA gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 ggatgtgagg gcatatggc tgccacatct gtcacccat tgcgtccag
51 gtttattcg gctgatctgg ctggtaggc ggggttcccc ttccctccctc
101 accgttccat gtgcgtccct cccaaagctg cgcgttcgtt cgaagaggac
151 gaccatcccc gatagaggag gaccggttt cggtaaggataacagata
201 gtcgttgtcc cctgttagaa cttccaaaca agctctcaag gtccatttg
251 aggagaacgt aggtagtca agttccaag actccagaca catccaaatg
301 aggccgttca tggcagtc tgcstttttt tt

DN 1 ANSWER 45 OF 62 CAPLUS COPYRIGHT 2005 ACS ON STN

Full Text

AN 1987:79526 CAPLUS

DN 106:79526

TI Structure and expression of the human calcitonin/CGRP genes

AU Steenbergh, P. H.; Hoppenre, J. W. M.; Zandberg, J.; Visser, A.; Lips, C.

J. M. Jansz, M. S.

Insu. Mol. Biol., Utrecht, 3508 TB, Neth.

ESIS Letters (1986), 202(1), 97-103

DO

CODEN: FEVIAL; ISSN: 0014-5733

JP Journal

IA English

AB The isolation of cDNA encoding a 2nd human calcitonin gene-related peptide (hCGRP-II) [98824-26-1] was previously reported. The isolation and characterization of the gene encoding hCGRP-II are described. This gene, designated CALC-II, is structurally closely related to the known CALC-I gene encoding human calcitonin (hCT) and hCGRP-I. In contrast to CALC-I, CALC-II does not seem to be alternatively expressed. The formation of a 2nd hCT-like mRNA by differential splicing of CALC-II transcripts is unlikely in view of the structure of CALC-II, and could not be demonstrated in tissues known to express CALC-I and CALC-II.

IT 106907-84-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106:79526 CAPLUS

CN DNA (human clone Cos2CALC-II gene CALC-II coding region) (9CI) (CA INDEX NAME)

SEQ 1 atgggttccc ggaaggttctc cccctttctgt gtcgttcgtt tcttggtct
51 gtaccaggcg ggcggccccc agggggcgcc attcagggtct gcccgtggaga
101 gtagccca gggccaca ctcgtttaaag aggacgcgtt cttccctgtt
151 gctgtactgg tgcaggacta tgcgttgcgtt aaggccgtt agctgttgc
201 ggagcaggag acacagggtt ccagtcgttcc tggccagaag agagcctgtca
251 acactgccac ctgtgttgcact catggcttgg caggcttgcgtt gagcgtatca
301 gggggcatgg tgaagagcaa ttctgttgcaccatgttgg gttccaaagc
351 ctggcagg cgccgcagg accttcaagc ctgttgc

STN Columbus

L61 ANSWER 46 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:44684 CAPLUS

DN 106:44684

TI Nucleotide sequence of the tra YALE region from IncFV plasmid pED208

AU Finlay, B. Brett; Frost, Laura S.; Paranchych, William

CS Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.

SO Journal of Bacteriology (1986), 168(2), 990-8

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CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB The pED208 plasmid is a 90-kilobase (kb) conjugative plasmid which is the derepressed form of F0 lac plasmid (IncFV). A 3.3-kb HindIII-PstI fragment from the pED208 plasmid was cloned and sequenced and was found to contain 4 open reading frames which were highly homologous to the traA, traL, traE, and traY gene products of the F plasmid. The pED208 traA propilin protein was 119 amino acids in length, consisting of a leader sequence of 55 amino acids and a mature pilin subunit of 64 residues. The leader sequence contained a hydrophobic region followed by a classic signal peptidase cleavage site (Ala-Ser-Ala-55). F and pED208 pilin proteins shared 27 conserved residues and had similar predicted secondary structures. The pED208 traA and traL genes were sep'd. by a single base pair and no ribosome binding site preceded the traL gene. The pED208 traY gene contained an IS2 insertion element in orientation II 180 nucleotides (60 residues) upstream of the traY stop codon. This insertion of IS2 resulted in a predicted fusion peptide of 69 residues for traY which may provide the obsd. traY activity. Since IS2 is absent in the wild-type plasmid, F0 lac, derepression and concomitant multipilation may be due to the insertion of IS2 providing constitutive expression of the pED208 tra operon.

GT 60389-661-4

RL F0B (Properties); BROW (Biological study)

(nucleotide sequence of)

RV 106383-05-4 CAPLUS

CN DNA (plasmid pED208 gene traA) (9CI) (CA INDEX NAME)

NTS double stranded

ORG 1. atgaaatttat cctttgcaaaa aggccggcctc cctgcgcctg taaaaaaaccg
50. tcgtatggcag tactgccatgt tggcatggcg cggtgtgacc agtaaaaaaaaag
100. cgtgttcggc tctggccatgt ctgtctccgc tgctttaact cgtgtgtggaa
150. gagatggcca gtgcacatgtc cctgcgtggcc gggggcaagg atgatgtgaa
200. ccacaccttc ggtggcgact cattcgtcatgtatgtatc atcattgtccg
250. ttctgttattgtt cgggtgtggcg atgtatatacc gcaccaagaat cctgtgtatc
300. ctgtgtggcc tgggtgttgt tatcgtcttc actaccgtcg gttttacattt
350. catcaaatgt

L61 ANSWER 47 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:535044 CAPLUS

DN 105:145044

TI Isolation of the human gene for bone gla protein utilizing mouse and rat cDNA clones

AU Calleste, A. J.; Rosen, V.; Suecker, J. L.; Kriz, R.; Wang, E. A.; Wozney,

STN Columbus

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|--------------------|------------|----------------|----------|
| AT 53237 | E 19900615 | AT 1985-301617 | 19850308 |
| PRAI JP 1984-44437 | A 19840308 | | |
| EP 1985-301617 | A 19850308 | | |

AB Enhancer elements are isolated from papovavirus BK mutants and are used to enhance the expression of cloned genes in host eukaryotic cells. Thus, viral DNAs were extd. from papovavirus BK mutants pm525, pm411, and pm522, and the HindIII-C fragment of each mutant was isolated, cloned into the phage vector mp8, and sequenced. The enhancer activity of each HindIII-C fragment was established by cloning the fragment into a plasmid pBR322 that already contains the herpes simplex type 1 virus thymidine kinase (TK) [9002-06-6] gene, plasmid pTK. The recombinant plasmids were introduced into mouse L (TK-) cells, and their expression was monitored. As a result, the HindIII-C DNA fragments of pm411, pm522, and pm525 viral DNAs showed 10.1-20-fold enhancement of transcription in mouse L (TK-) cells over the control. This activity was exhibited irresp. of the orientation, distance, or position of the HindIII-C DNA fragment.

IT 99533-38-7 99533-39-8 99533-40-1

RL: PPR (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 99533-38-7 CAPLUS

CN DNA (BK virus strain pm411 enhancer element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 cctttgtcca gtttaactat taactgcccac tggctgctgc ccagtcatgc
51 acatttccttc ctgaggcata ggctggctgc ccagtcatgc acttcccttc
101 ttgaggcgtg cccagtcata ctgaggcata ggctggctgc ccagtcatgc
151 acatttccttc ctgaggcgtg cccagtcata cactttccctt cctgaggcata
201 cggttttggct gcattccatg ggttaaggcagc tcctccctgt gg

RN 99533-39-8 CAPLUS

CN DNA (BK virus strain pm522 enhancer element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 cctttgtcca gtttaactat taactgcccac tggctggctg cccagtcata
51 acatttcctt cctgaggcata tggtggctg cccagtcata cactttccct
101 ttgaggcgtg gcccagtcata gcactttccct tcctgaggcata atggtttgcc
151 tgcattccat gggtagcagc tcctcccttg tgg

RN 99533-40-1 CAPLUS

CN DNA (BK virus strain pm525 enhancer element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 cctttgtcca gtttaactat taactgcccac tggctggctg cccagtcata
51 acatttcctt cctgaggcata tggtggctg cccagtcata cactttccct
101 ttgcccagttt taactataaaac tgccactygc tggctccct agtcatgcac
151 ttcccttcct gagggcgtgcc tagtcata gca ctttccttcc tgaggcata
201 ttggcgtgc attccatggg taaggcagc tcctccctgtgg

STN Columbus

TI DNA sequence and characterization of the *Escherichia coli* serB gene
AU Neuwald, Andrew F.; Stauffer, George V.
CS Dep. Microbiol., Univ. Iowa, Iowa City, IA, 52242, USA
SO Nucleic Acids Research (1985), 13(19), 7025-39

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CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The sequence of a DNA fragment contg. the *E. coli* serB gene was detd. An open reading frame of 966 nucleotides was identified that encodes a polypeptide of 322 amino acids with a mol. wt. of 35,002 daltons. The transcription start site was detd. by Mung Bean nuclease mapping. The -10 and -35 regions of the serB promotor lack homol. to the consensus sequences. In addn., the -35 region of the serB promoter overlaps the -35 region of a 2nd divergent promoter. Frameshift mutations were constructed at 3 different sites within the serB gene. When plasmids carrying these mutations were used as templates in a minicell system, mutations closer to the proposed transcription and translation start sites resulted in smaller polypeptides than did those further away, confirming the proposed direction of transcription and translation. The obsd. sizes of the truncated and native polypeptides were in agreement with those predicted from the DNA sequence. A very stable stem and loop structure ($\Delta G = -32$ kcal/mol) that does not fit the criteria of known transcription terminators was found one nucleotide downstream from the putative UAA translation stop codon.

IP 99549-64-1

RL: PPF (Properties); BIOL (Biological study)

(nucleotide sequence etc)

REI 99549-64-1 CAPLUS

CN DNA (*Escherichia coli* clone pSS154 gene serB) (9CI) (CA INDEX NAME)

MIS double stranded

NES

SEQ 1 atcccttaaca ttacgtggtg cgaccttcgtt gaagaatgtct ctttatggcc
51 ggytctgcct cttrattaa gtgggtatga aatgtatgccca ctggattacc
101 acgcaggctcg tagcggctgg ctgtctgtatg gtctgtggct ggataaaacaa
151 cytctgaaaa aataccagag caaactgggt gcggcgatgg tgattgttc
201 cggctggtc gtggaaagatt atcaggtat tcgtctggca ggtrcaactca
251 ccgcacgggc tacacgcctg gcccacgaag cgccagctgga tggcgcggc
301 ctggggaaaa tcccccacct gcgcacgcgg cgggtttgtct ggtga-

L61 ANSWER 50 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

DPL Text

AN 1005:499559 CAPLUS

DA 100:99659

TC Structure of the *Escherichia coli* S10 ribosomal protein operon

AU Zurawski, Gerard; Zurawski, Sandra Marvo

CS DNAX Res. Inst. Mol. Cell. Biol., Palo Alto, CA, 94304, USA

SO Nucleic Acids Research (1985); 13(12), 4521-6

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CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB The complete structure of the *E. coli* S10 ribosomal protein operon is presented. Based on the DNA sequence, the deduced order of the 11 genes in the operon is rpsJ, rplC, rplD, rplW, rplB, rpsS, rplV, rpsC, rplP, rymC, rpsQ. The estd. transcribed length of the operon is 5181 base pairs. Putative sequences involved in ribosome binding are discussed. The DNA sequence data corrects several errors in previously detd. protein

STN Columbus

sequence data.

IT 80451-23-6

RL: PRP (Properties)
(nucleotide sequences of)

RN 80451-23-6 CAPLUS

CN DNA (Escherichia coli ribosome protein S 10 gene) (9CI) (CA INDEX NAME)

SEQ 1 atgcagaacc aaagaatccg tatccgcctg aaagcggtt g atcatcgatct
51 gatcgatcaa gcaaccgcgg aaatcgatcg aactgccaag cgcaactggtg
101 cgcaggatccg tggccgcata ccgcgtccga cacgcaaaga ggcgttcact
151 gttctgatct ccccgacgt caacaagac ggcgcgcata agtacgaaat
201 ccgtactcac ttgcgtctgg ttgacatcg tgagccaacc gagaaaaccg
251 ttgatgatct gatgcgtctg gatctggctg ccgggtgtaga cgtgcagatc
301 agccgtggtt aa

L61 ANSWER 51 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:482528 CAPLUS

DN 103:82528

TI Nucleotide sequence of the alpha ribosomal protein operon of Escherichia coli

AU Bedwall, David; Davis, Geneva; Gosink, Mark; Post, Leonard; Nomura, Masayasu; Kestler, Harry; Zengel, Janice M.; Lindahl, Lasse

JS Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA

SG Nucleic Acids Research (1985), 13(11), 3891-903

DOI NARHAD; ISSN: 0305-1043

AB

AB In E. coli some 19 transcription units encoding the 52 ribosomal proteins are scattered throughout the genome. One of the units, the α operon, encodes genes for the ribosomal proteins S13, S11, S4, and L17 as well as the kilobase subunit of RNA polymerase. [9014-24-8]. The complete 5.3-kilobase nucleotide sequence of the α operon is reported. In addition, the site of transcription termination in this operon was detd.

IT 57708-10-5

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 57708-10-6 CAPLUS

CN DNA (Escherichia coli ribosome protein S 13 gene) (9CI) (CA INDEX NAME)

SEQ 1 tggggccgtta tagcaggcat taacattctt gatcataagg atgcccgtaat
51 tggcattaaact tggatttatg gcgtcggcaa gaccgttctt aaaggccatcc
101 tggctgcggc gggtatcgat gaagatgtt agatcgtgtt gctgttgtaa
151 ggacaaatcg acacgtcgat tgacgaaatg gccaattttt tcgttgaagg
201 tttatctgcgc cgtaaaatca gcatgagat caaggccctg atggatctt
251 tttgtgtatcg cggtttgcgtt catcgatcgat gtctcccggt tcgcggtcag
301 cgttaccaaga ccaacgcacg taccggtaag ggtccggca aaccgatc
351 guaataaa

L61 ANSWER 52 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:432882 CAPLUS

DN 103:32882

STN Columbus

TI Alternative RNA processing events in human calcitonin/calcitonin gene-related peptide gene expression
AU Jonas, Vivian; Lin, Chijen R.; Kawashima, Eric; Semon, Dominique; Swanson, Larry W.; Mermod, Jean Jacques; Evans, Ronald M.; Rosenfeld, Michael G.
CS Sch. Med., Univ. California, La Jolla, CA, 92093, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1985), 82(7), 1994-8

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CCDEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB Two mRNAs generated as a consequence of alternative RNA processing events in expression of the human calcitonin [9007-12-9] gene encode the protein precursors of either calcitonin or calcitonin gene-related peptide (CGRP) [83652-28-2]. Both calcitonin and CGRP RNAs and their encoded peptide products are expressed in the human pituitary and in medullary thyroid tumors. Apparently, both the calcitonin and CGRP exons arose from a common primordial sequence, suggesting that duplication and rearrangement events are responsible for the generation of this complex transcription unit.

IT 95827-33-7

RL: ERP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 95827-33-7 CAPLUS

CN DNA (human clone pCGRPH1 calcitonin gene-related peptide cDNA) (9CI) (CA
THERAPY NAME).

NM: Double-stranded

SEI 1 acgggtttcc aaaagtttctc ccccttcctg gctctcayca tcttgggtct
31 ggtgcaggca ggcagccccc atgcagcacc attcagggtctt gcctggaga
601 gtagcccaac agacccggcc acgcgtcaggc aggacaaacgc gcgcctccgt
901 ccggctgcac tgggtcgagga ctatgtcgag atgaaggycac gtgagctgg
211 ggaggagccaa yagagagagg gctccaaatattgcccac aagagagacct
251 acactgtc caccctgtgc actcatcgcc tggcagggtt gctyagcaga
301 tgggggttgggtt aagaaa caactttgtt cccaccaatgtt tggttccaa
351 Aggtttggcc agggccggca gggacatcca agccgtgt

LET ANSWER-63 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

JNL Text

AV 1983/11/120.. CAPLUS

DN 95827-33-70

TI Cloning and characterization of a mRNA-encoding rat preprosomatostatin
AU Rogers, Christie L.; Minth, Carolyn D.; Deschenes, Robert; Magazin,
Magil, N.; Tavianini, Marie A.; Sheets, Mike; Collier, Kenneth; Weith, H.
Aron, David C.; et al.

CS Dep Biochem., Purdue Univ., West Lafayette, IN, 47907, USA

SO Journal of Biological Chemistry (1983), 258(14), 8781-7

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CCDEN: JBCHA3; ISSN: 0021-9253

DT Journal

LA English

AB An oligonucleotide extended hybridization probe was used to screen a rat medullary thyroid carcinoma cDNA library for clones which contain preprosomatostatin [75037-28-4] sequences. The nucleotide sequence encoding rat preprosomatostatin is reported. The sequence of cDNA contains 67 nucleotides in the 3'-noncoding region, 84 nucleotides in the 5'-untranslated region, and 458 bases corresponding to the coding region. The mRNA codes for a somatostatin precursor of 116 amino acids (mol. wt.

STN Columbus

12,773). The preprosomatostatin has a sequence of hydrophobic amino acids at the N terminus, which is followed by a peptide of ~78 residues, which precedes somatostatin-14 [51110-01-1]. The amino acid sequences of rat and human preprosomatostatin differ by only 4 amino acid residues. Translation of rat poly(A) RNA in a rabbit reticulocyte cell-free system followed by immunopptn. with antisera directed against somatostatin-14 demonstrated the synthesis of a single protein of mol. wt. 15,000. Two proteins, of mol. wts. 14,000 and 15,000, are immunopptd. from a wheat germ cell-free translation mixt. Northern anal. of the somatostatin mRNA indicated that it is of ~850 nucleotides. Anal. of several medullary thyroid carcinomas demonstrated that 1 tumor, designated WF, had immunoreactive somatostatin-14 in concns. of 350 ng somatostatin-14/mg protein and somatostatin mRNA that represented 10% of the cellular poly(A) RNA. Cell lines derived from this tumor might provide an attractive system to investigate the regulation of somatostatin gene expression.

IT 86090-46-2

RL: PRF (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 86090-46-2 CAPLUS

CN DNA (rat somatostatin cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgctgtcct gccgtctcca gtgcgcgtc gcccgcgtct gcacatcgcttc
51 ggctttggc ggtgtcaccc gggcgccctc ggaccggaga ctccgtcagt
101 ttccggcagaa gtctctggcg gctgccaccg ggaaacagga actggccaaag
151 ttttttttgg cagaactgtct gtctgagccc aaccagacag agaacatgtc
201 ccggggcct gaggatrtgc cccaggcgc tgagcaggac gagatgaggc
251 tggcggtc gagggtgtcc aactctgaacc cagccatggc accccgggaa
301 tggcgaaatgt gctgcaagaa sttcttctgg aagacattca catccgtta
351 g

LET NUMBER 54 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN.

Full Text

AC 1983A-433821 CAPLUS

DN S9:33821

TI Rat prostatic steroid binding protein: DNA sequence and transcript maps of the two C3 genes

AU Eustace, M. G.; Parker, M. G.

CS Inst. Cancer Res., London, WC2A 3PX, UK

SO EMBO Journal (1983), 2(5), 769-74

====

CODEN: EMJODG; ISSN: 0261-4189

JPIC Journal

Engl Edn

AB In the rat, there are 2 nonallelic genes, C3(1) and C3(2), for the C3 polypeptide and prostatic steroid-binding protein. Both genes were cloned and sequenced. Only C3(1) is responsible for the prodn. of authentic C3. Although there is a marked difference in their transcriptional activity, the 2 genes share extensive DNA sequence homol., there being only 1 base difference from nucleotide -235 to within the 1st intron. Transcript mapping showed that there are 2 distinct C3 transcripts which share a unique 3' terminus but have 5' termini 38 bases apart, each preceded by a TATA box homol. An identical repetitive element is present just upstream of both genes. Both families of transcripts, which are produced in a ratio of 18:1, are coordinately related by testosterone.

IT 86090-46-2 86243-28-9

RL: PRF (Properties); BIOL (Biological study)
(nucleotide sequence of)

STN Columbus

RN 84789-32-2 CAPLUS
CN DNA (rat prostatein subunit C3 cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagctgg tgtttctatt ctgttggtc accatcccta tttgctgcta
51 tgccagggtt cttggctgca gtattctaga tgaagtttatt agaggtacaa
101 ttaactcaac tgtgacttta catgactata taaaatttagt taagccatat
151 gtacaagatc atttactgtaaaggctgtg aagcaattca agcagtgtt
201 tctagatcg accgacaaga ctctggaaaa ttttggcgtg atgatggagg
251 caatatttaa cagtgaaagc tgtcaacagc catcctaa

RN 86243-28-9 CAPLUS
CN DNA (rat prostatein subunit C3(2) gene coding region) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagctgg tgtttctatt ctgttggtc accatccccca tttgctgcta
51 tgccagggtt cttggctgca gtattctaga tgaagtttatt agaggtacaa
101 ttaattcaac tgtgacttta catgactata taaaatttagt taagccatat
151 gtacatgtatc atttactgtaaatgctgtg aagcaattca agcagtgtt
201 tctagatcg accaacaaga ctgttggaaaa ttttggcgtg atgacggagg
251 caatatttaa cagtgaaagc tgtcaacagc catcctaa

661 ANSWER 65 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AB 86091-26-1 CAPLUS

DB 8616707

TI Rat pre-prosomatostatin. Structure and processing by microsomal membranes

AR Goodwin, Richard H.; Aron, David C.; Roos, Bernard A.

GS Lab. Mol. Endocrinol., Massachusetts Gen. Hosp., Boston, MA 02111, USA

SO Journal of Biological Chemistry (1983), 258(9), 5570-3

====

CODEN: JBCHA3; ISSN: 0021-9258

DT Original

LA English

AB The complete sequence of rat preprosomatostatin [86091-26-1], deduced from the nucleotide sequence of cDNAs derived from a somatostatin-rich medullary thyroid carcinoma is presented. Rat preprosomatostatin contains 116 amino acids (12,737 daltons). Cell-free translations of medullary thyroid carcinoma mRNA with dog pancreas microsomal membranes were performed to identify the cleavage point of the leader region from preprosomatostatin. Partial microsequencing data indicates that the cleavage occurs between the glycine and alanine at positions 24 and 25 of preprosomatostatin. Thus, rat prosomatostatin [86093-95-4] contains 92 amino acids (10,388 daltons). Comparison of the amino acid sequences of the rat and human preprosomatostatins reveals only 4 amino acid substitutions. The high level of conservation between rodents and humans of the entire preprosomatostatin mol. further suggests the possibility of biological junctions of the NH₂-terminal portions of prosomatostatin.

IT 86093-95-4

AB: EXP (Properties)

(nucleotide sequence of)

RN 86093-95-2 CAPLUS

CN DNA (rat somatostatin cDNA) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

SEQ 1 atgctgtcct gccgtctcca gtgcgcycgtg yccgcgcctc gcatcgctt
51 gyctttgggc ggtgtcaccc gggcgccctc ggacccaga ctccgtca
101 ttctgcagaa gtctctggcg gtcgcaccgg gaaacaggaa actggca
151 tacttcttgg cagaactgtct gtctgagccc aaccagacag agaacatgc
201 cctggaggcct gaggatttgc cccaggcagc tgagcaggac gagatgaggc
251 tggagctgca gaggtctgcc aactcgaacc cagccatggc accccggaa
301 cgcaaagctg gctgcaagaa cttcttctgg aagacattca catctgtta
351 g

L61 ANSWER 56 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:102042 CAPLUS

DN 98:102042

TI Prostatic steroid-binding protein. Isolation and characterization of C3 genes

AU Parker, Malcolm G.; White, Roger; Hirst, Helen; Needham, Maurice; Tilly, Rita

CS Imp. Cancer Res. Fund, London, WC2A 3PX, UK

SC Journal of Biological Chemistry (1983), 258(1), 12-15

=====

CODE: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB Prostatic steroid-binding protein, the expression of which is stimulated by estrogens, consists of 2 subunits, 1 contg. the polypeptides C1 and C3, and the other contg. the polypeptides C2 and C3. C3 mRNA-specific cDNA clones were isolated, sequenced, and used to isolate and characterize genomic clones for 2 C3 genes. Both genes are 3.2 kilobases with identical exon/intron arrangements; this is similar to the organization of C1 and C2 genes, which suggests that they might have arisen by derivations of an ancestral gene. Homologous human genes were not detected.

PR 98:102042

CDR (Properties); BIOL (Biological study)

CC (Nucleotide sequence of)

PR 64739-32-2 CAPLUS

CN RNA (rat prostatein subunit C3 cDNA) (SCI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagctgg tttttttttt ttgttgttgc accatccata tttgttgtca
51 tgccatgtgt tttttttttt ttgttgttgc aatattttagt tggatgttacaa
101 ttaactcaat tttttttttt tttttttttt tttttttttt tttttttttt
151 gtacaaatgtt tttttttttt tttttttttt tttttttttt tttttttttt
201 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
251 caataatttaa tttttttttt tttttttttt tttttttttt tttttttttt

L61 ANSWER 57 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:47849 CAPLUS

DN 98:47849

TI Alternative RNA processing in calcitonin gene expression generates mRNAs encoding different polypeptide products

AU Amara, Susan G.; Jonas, Vivian; Rosenfeld, Michael G.; Ong, Estelita S.;

STN Columbus

Evans, Ronald M.
CS Div. Endocrinol., Univ. California Sch. Med., San Diego, CA, 92093, USA
SC Nature (London, United Kingdom) (1982), 298(5871), 240-4

=====
CODEN: NATUAS; ISSN: 0028-0836

DT Journal

LA English

AB Alternative processing of RNA transcripts from the calcitonin gene resulted in the prodn. of distinct mRNAs encoding the hormone calcitonin [9007-12-9] or a predicted product referred to as calcitonin gene-related peptide (CGRP) [83652-28-2]. The calcitonin mRNA predominated in the thyroid whereas the CGRP-specific mRNA appeared to predominate in the hypothalamus. A model is proposed in which developmental regulation of RNA processing is used to increase the diversity of neuroendocrine gene expression.

IT 83667-67-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 83667-67-8 CAPLUS

CN DNA (rat hypothalamus preprocalcitonin gene-related peptide cDNA) (9CI)
(CA INDEX NAME)

NF doublestranded

SEQ:
1 atgggttttc tyaagttctc ccctttccctg gttgtcagca tcttgctct
51 gtaccaggca tgccgcctcc aggcaattcc tttgaggta accttagaaa
101 gcagccagg catggccact ctcaatcgaa aagaagctcg cctactggct
151 tcactgggtgc tgaactataat gcagatgaaa gtcaggggagc tggagcagga
201 ggaggaaacag gaggttgacy gtcataagat cactggccag aagagatcct
251 tcacacactgc taccctgcgtg accccatcgcc tggcaggctt gctgagcagg
301 tccggggatgt tggtaggatcaatttgtt cccaccaatg tgggctctga
351 agccttcggcc cggccgcggca gggacccatca ggcttga

AMERICAN SECTION 58 OF 62 CAPLUS COPYRIGHT 2005 ACS ON STN

AM 1982:556654 CAPLUS

DBI 97-556654

TI Human somatostatin I: sequence of the cDNA

AU Shen, Yu Ping; Pictet, Raymond L.; Rutter, William J.

DEP Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1982), 79(15), 4575-9

=====
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB mRNA has been isolated from a human pancreatic somatostatinoma and used to prep. a cDNA library. After prescreening, clones contg. somatostatin sequences were identified by hybridization with an anglerfish somatostatin 1-cloned cDNA probe. From the nucleotide sequence of 2 of these clones, an essentially full-length mRNA sequence, including the preprosomatostatin-coding region, 105 nucleotides from the 5' untranslated region and the complete 150-nucleotide 3' untranslated region, have been deduced. The coding region predicts a 116-amino acid precursor protein [83271-75-4] (Mr, 12,727) that contains human somatostatin I [40958-31-4] and -28 [75306-06-8] at its COOH terminus. The predicted amino acid sequence of human somatostatin-28 is identical to that of somatostatin-28 isolated from the porcine and ovine species. A comparison of the amino acid sequences of human and anglerfish preprosomatostatin I indicated that

STN Columbus

the COOH-terminal region encoding somatostatin-14 and the adjacent 6 amino acids are highly conserved, whereas the remainder of the mol., including the signal peptide regions, is more divergent. However, many of the amino acid differences found in the pro region of the human and anglerfish proteins are conservative changes. This suggests that the propeptides have a similar secondary structure, which in turn may imply a biol. function for this region of the mol.

IT 83270-98-8

ARL: PRF (Properties)
(nucleotide sequence of)

RN 83270-98-8 CAPLUS

CN DNA (human preprosomatostatin I cDNA) (9CI) (CA INDEX NAME)

SEQ 1 atgctgtcct gcccctcca gtgcgcgtg gtcgcgtgt ccatcggtcct
51 ggcctggc tttgttaccgg ggcgtccctc ggacccaga ctccgtcagt
101 ttctgcagaa gtcctggct gtcgcgcgg ggaaggcagga actggccaag
151 ttttttttggcagagctgt gtcgttgcacc aaccagacgg agaatgtatgc
201 cctggAACCT gaagatctgt cccaggctgc tgagcaggat gaaatgaggc
251 tttagctgca gagatctgt aactcaaacc cggctatggc acccccggagaa
301 cggaaagctg gtcgtcaagaa ttttttctgg aagacttca catcctgtta
351 g

661 ANSWER 59 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

FROM 1981-08-21 1981-08-21

AS 1981-08-21 1981-08-21 CAPLUS

AT 37-1981

CC Somatostatin or somatostatin precursors

AN Hobbs; Rener; Crawford, Robert; Pictet, Raymond L.; Rutter, William J.

DA University of California, Berkeley, USA

SOU US Pat. Appl., 50 pp.

C07H 11/00 KWDW

PT Pat.

PL Englis

PPN C07H 11/00

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE | PALANT |
|------------------|------|----------|---|--------------|----------------|
| EP 466639 | A1 | 19820303 | EP 1981-303825 | 19810821 <-- | EP 1981-303825 |
| EP 466639 | B1 | 19841024 | | | EP 1981-303825 |
| EP 466639 | | | RK AT; BE, CH, DE, FR, GB, IT, LU, NL, SE | | |
| ZA 3105671 | A | 19820825 | ZA 1981-5671 | 19810817 <-- | ZA 1981-5671 |
| IL 51673 | A1 | 19850630 | IL 1981-63629 | 19810820 <-- | IL 1981-63629 |
| FI 81A2593 | A | 19820226 | FI 1981-2593 | 19810821 <-- | FI 1981-2593 |
| AT 303825 | E | 19841115 | AT 1981-303825 | 19810821 <-- | AT 1981-303825 |
| DK 19810827 | A | 19820226 | DK 1981-3727 | 19810824 <-- | DK 1981-3727 |
| AU 744178 | A1 | 19820304 | AU 1981-74478 | 19810824 <-- | AU 1981-74478 |
| JP 544147 | B2 | 19860206 | | | JP 544147 |
| JP 5441455 | A2 | 19820806 | JP 1981-133229 | 19810824 <-- | JP 5441455 |
| ES 504919 | A1 | 19830101 | ES 1981-504929 | 19810824 <-- | ES 1981-504929 |
| HU 19810829 | O | 19840228 | HU 1981-2454 | 19810824 <-- | HU 1981-2454 |
| DD 2030451 | A5 | 19830914 | DD 1981-232787 | 19810825 <-- | DD 1981-232787 |
| ES 504928 | A1 | 19830416 | ES 1982-514528 | 19820729 <-- | ES 1982-514528 |
| PRAL 1980-181046 | A | 19800825 | | | |
| EP 1981-303825 | A | 19810821 | | | |

AP The sequences for somatostatin and its precursors are cloned. Thus, poly(A)-contg. RNA was isolated from Brockmann bodies of the anglerfish (*Lophius americanus*) and used as a template to synthesize cDNA, which was subsequently provided with dC tails. Plasmid pBR322 was cleaved by restriction endonuclease PstI and provided with dG tails. Equimolar amts.

STN Columbus

of dG-tailed cDNA and dG-tailed pBR322 were annealed and used to transform *Escherichia coli* λ 1776, and tetracycline-resistant transformants were selected. Transformants contg. anglerfish sequences were identified by colony hybridization, with a ^{32}P -labeled cDNA synthesized from anglerfish Brockmann body poly(A)-contg. RNA as probe. Purified insert cDNAs from 2 of the colonies were sequenced. One recombinant plasmid (pLaS1) contained DNA coding for preprosomatostatin [75037-28-4]-1; another (pLaS2) coded for somatostatin [51110-01-1]-2. DNA sequences coding for prosematostatin [74315-46-1]-1, preprosomatostatin-2, and prosomatostatin-2 were also cloned.

IT 77000-19-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 77000-19-2 CAPLUS

CN DNA (*Lophius americanus* preprosomatostatin II cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgcagtgtta tccgttggcc cgccatcttg gcttcctcgg cgttgggttct
51. gtgcggccca agtgtttctt cccagctcgaa cagagacgac aacacc
101. aggacaccttggaa cctggagactg cgtcagact ggctgttggaa gagagccccgg
151. agcgcggacac tcctgtccca ggatggaggaa aaacggccgg tggaggagct
201. gctggcttag atgtctctgc cagaggccac gttccagccgg gaggccggagg
251. acgcgtccat ggcaacagaa ggacggatga acctagagcg gtcgcgtggac
301. tcttaccaaca acctaaaaaaa tctgtgagcgt aaagctggct gtaagaactt
351. ctatttggaaag gggttcaactt cctgt

ANSWER 60 OF 62 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 77000-19-2 CAPLUS

DN 95-10-4132

TI Overlap between ampC and frd operons on the *Escherichia coli* chromosome

AU Sandstroem, Thomas; Jaurin, Bengtakke

CS *J. Microbiol.*, Univ. Umeaa, Umeaa, S-901 87, Swed.

SP *Proceedings of the National Academy of Sciences of the United States of America* (1982), 79(4), 1111-15

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CODEN: PNAS6; ISSN: 0027-8424

DT Journal

LA English

AB The promoter for the *E. coli* ampC β -lactamase [9073-60-3] gene is located within the last gene of the fumarate reductase [9076-99-7] (frd) operon. Evidently, the ampC attenuator serves as the terminator for transcription of this preceding operon. The nucleotide sequence was detd. for 2 proteins that are encoded by a DNA segment preceding the ampC gene. The 2 proteins consisted of 131 and 119 triplets and had mol. wts. of 15,800 and 13,100, resp. The 12 COOH-terminal amino acids of the 13,100-dalton protein overlapped the ampC promoter. Accordingly, a G-C insertion in the promoter gave both increased transcription of ampC and a frameshift in this overlapping gene, resulting in readthrough proteins. Thus, a type of very compact genetic organization of operons in prokaryotes is described.

IT 81669-91-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 81669-91-0 CAPLUS

CN DNA (*Escherichia coli* frd operon 13.1-kilodalton protein gene) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

SEQ 1 atgattaatc caaatccaaa gcgttctgac gaaccggtag tctyggggcc
51 cttcgcccccc ggtggtatgt ggagcccat catggccgg gtatgtatcc
101 tgctgggtggg tattctgctg ccactggggt tgttccggg tgatgcgtg
151 ayctacgagc gcyttctgye gttegcgcag aycttcattg gtcgcgtatt
201 cctgttcctg atgatcggtc tgccgctgtg gtgtggttta caccgtatgc
251 accacgcgat gcacgatctg aaaatccacg tacctgcggg caaatgggtt
301 ttctacggtc tggctgtat cctgacagtt gtcacgctga ttggtgtcgt
351 tacaatctaa

L61 ANSWER 61 OF 52 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982:46833 CAPLUS

DN 96:46833

TI Regulation of the S10 ribosomal protein operon in *E. coli*: nucleotide sequence at the start of the operon

AU: Olin's, Peter O.; Nomura, Masayasu

CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA

SO Cell (Cambridge, MA, United States) (1981), 26(2, Pt. 2), 205-11

三

CODEN: CELLB5; ISSN: 0092-8674

PT Journal

LA English

AB The DNA sequence of a 1250-base-pair segment of the *Escherichia coli* chromosome that carries the promoter for the S10 ribosomal protein operon, the S10 gene, and part of the L3 gene was detd. A DNA fragment carrying the negative S10 promoter was cloned into the plasmid mini-Col E1, which contains a transcription termination signal close to the single HindII site. Cells harboring the hybrid plasma produced a relatively stable hybrid mRNA with the expected sequence, demonstrating that the promoter functions *in vivo*. Comparison of the mRNA sequence around the start of the S10-coding region, the presumed target site for L4 repressor protein, with the known binding site for L4 on 23S rRNA revealed the presence of several homologies. This supports the model of the translational feedback regulation of the S10 operon by L4.

J2 80451-23-6

PRO (Properties); BIOL (Biological study)

(nucleotide sequence of)

129 96431423-6 CAPLUS

CM - DNA (Escherichia coli ribosome protein S 10 gene) (9CI) : (CA INDEX NAME)

SEQ 1: tgcggaaaacc taagaatccg tttccgtctg taatcggttcg atcatcgct
 11: ttatcgatcattt gchaaacgcgg aaatccgtcg gactgccaag cgcactggtg
 161: ccgagggtccg tggtcgcattt ccgcgtccga taatccaaaga ggcgttcaat
 153: ttgttcgtatcttccccgeasgtt caacaaagac tcgtcgatc agtacgaat
 202: ccgttactcad ttgtcgatcg ttgacatgtt ccggccaaacc gagaaaaacgg
 251: ttgtatgtctt gatcgatctg gatctggctg ccggtgtttaga cgtgcagatc
 301: agccgtgggtt aa

661 ANSWER 62 OF 62 CAP1.US COPYRIGHT 2005 ACS on STN

Page 11 Text

ABT 1937-134404 CAPLUS

BN 94-134404

TI Cloning and sequence analysis of cDNAs encoding two distinct somatostatin

STN Columbus

AU precursors found in the endocrine pancreas of anglerfish
Hcbart, Peter; Crawford, Robert; Shen, Lu Ping; Pictet, Raymond; Rutter,
William J.
CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA
SO Nature (London, United Kingdom) (1980), 288(5787), 137-41

CODEN: NATUAS: ISSN: 0028-0836

DT Journal

LA English

AB Complementary DNAs for 2 distinct anglerfish (*Lophius americanus*) somatostatin peptides (I and II) were cloned in bacterial plasmids and sequenced. The nucleotide sequence for somatostatin I encoded a large precursor peptide (mol. wt. 13,300) in which the somatostatin hormone was at the carboxyl terminus. The predicted 14-amino acid sequence for anglerfish somatostatin I was the same as mammalian somatostatin. Somatostatin II was also formed as part of a larger precursor (mol. wt. 14,100) with the presumptive somatostatin hormone also at the carboxyl terminus. The 14-amino acid sequence of somatostatin II differed from somatostatin I at 2 internal residues (tyrosine in place of phenylalanine 7 and glycine in place of threonine 10). The 2 different somatostatins may have distinct biol. activities. Homologies in the amino acid sequences of the 2 peptides outside the somatostatin moiety suggested that other regions of the mols. may have biol. functions.

IT 77000-19-2

RL: PRP (Properties)
(nucleotide sequence cf)

PN 77000-19-2 CAPLUS

(*Lophius americanus* preprosomatostatin II cDNA) (9CI) (CA INDEX NAME)

new doublestranded.

=> \hat{a} has

(FINGER HOME) ENTERED AT 15:37:06 ON 29 APR 2005)

WIL 'REGISTRY' ENTERED AT 15:37:19 ON 29 APR 2005

| | | | |
|----|------|---|--------------------|
| L1 | 0 | S | CTGGCTGC/SQEN |
| L2 | 0 | S | CTGGCTGCCT/SQEN |
| L3 | 0 | S | CTGGCTGCCTGGG/SQEN |
| L4 | 3015 | S | CTGGCTGCCTGGG/SQSN |
| L5 | 190 | S | L4 AND SQL<=375 |

U.S. GOVERNMENT PRINTING OFFICE : 'APLUS' ENTERED AT 15:41:43 ON 29 APR 2005

| | |
|-----|--------------------|
| L6 | 0 S L5 AND PY<1990 |
| L7 | 1010 S L4 |
| L8 | 3 S L7 AND PY<1990 |
| L9 | 106 3 L5 |
| L10 | 0 S L5 AND PY<1991 |
| L11 | 0 S L9 AND PY<1991 |

STN Columbus

FILE 'REGISTRY' ENTERED AT 15:45:39 ON 29 APR 2005
L12 0 S TCACCAGCCC/SQEN
L13 78505 S TCACCAGCCC/SQSN

FILE 'CAPLUS' ENTERED AT 15:46:49 ON 29 APR 2005
L14 7141 S L13
L15 64 S L14 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:48:16 ON 29 APR 2005
L16 5749 S L13 AND SQL<400

FILE 'CAPLUS' ENTERED AT 15:48:46 ON 29 APR 2005
L17 1318 S L16
L18 2 S L17 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:50:45 ON 29 APR 2005
L19 0 S TTCATTGACG/SQEN
L20 21130 S TTCATTGACG/SQSN
L21 0 S TTCATTGATG/SQEN
L22 94859 S TTCATTGATG/SQSN
L23 6265 S L22 AND SQL<400

FILE 'CAPLUS' ENTERED AT 15:53:46 ON 29 APR 2005
L24 1521 S L23
L25 1 S L24 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:51:22 ON 29 APR 2005
L26 0 S CATCAGTCGG/SQEN
L27 50750 S CATCAGTCGG/SQSN
L28 4611 S L27 AND SQL<400

FILE 'CAPLUS' ENTERED AT 15:55:37 ON 29 APR 2005
L29 1311 S L28
L30 3 S L29 AND PY<1990

FILE 'REGISTRY' ENTERED AT 15:58:06 ON 29 APR 2005
L31 0 S TGCTCTCCAG/SQEN
L32 89727 S TGCTGTCCAG/SQSN
L33 6562 S L32 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:00:16 ON 29 APR 2005
L34 1650 S L33
L35 1 S L34 AND PY<1990

FILE 'REGISTRY' ENTERED AT 16:01:17 ON 29 APR 2005
L36 0 S GTTCGATGAG/SQEN
L37 23723 S GTTCGATGAG/SQSN
L38 1949 S L37 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:03:02 ON 29 APR 2005
L39 575 S L38
L40 2 S L39 AND PY<1990

FILE 'REGISTRY' ENTERED AT 16:04:42 ON 29 APR 2005
L41 0 S GGCCTCTGC/SQEN
L42 96510 S GGCCTCTGC/SQSN
L43 8374 S L42 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:06:32 ON 29 APR 2005
L44 1768 S L43
L45 2 S L44 AND PY<1990

STN Columbus

FILE 'REGISTRY' ENTERED AT 16:09:19 ON 29 APR 2005

L46 0 S AGACCGCGTC/SQEN
L47 13729 S AGACCGCGTC/SQSN
L48 1216 S L47 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:11:18 ON 29 APR 2005

L49 278 S L48
L50 1 S L49 AND PY<1990

FILE 'REGISTRY' ENTERED AT 16:12:10 ON 29 APR 2005

L51 0 S ACAGGGAAGT/SQEN
L52 63875 S ACAGGGAAGT/SQSN
L53 4067 S L52 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:13:55 ON 29 APR 2005

L54 1146 S L53
L55 1 S L54 AND PY<1990
S CTGGCTGC/SQEN

FILE 'REGISTRY' ENTERED AT 16:15:32 ON 29 APR 2005

L56 0 S CTGGCTGC/SQEN

FILE 'CAPLUS' ENTERED AT 16:15:33 ON 29 APR 2005

L57 0 S L56

FILE 'REGISTRY' ENTERED AT 16:16:01 ON 29 APR 2005

L58 106.010 S CTGGCTGC/SQSN
L59 111591 S L58 AND SQL<400

FILE 'CAPLUS' ENTERED AT 16:17:28 ON 29 APR 2005

L60 6350 S L59
L61 62 S L60 AND PY<1990

--> log v

COST IN U.S. DOLLARS

| SINCE FILE ENTRY | TOTAL SESSION |
|------------------|---------------|
| 491.29 | 1097.57 |

TOTAL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

| SINCE FILE ENTRY | TOTAL SESSION |
|------------------|---------------|
| -45.26 | -57.67 |

CA SUBSCRIBER PRICE

50. INTERNATIONAL LOGOFF AT 16:36:52 ON 29 APR 2005

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NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 FEB 25 CA/CAPLUS - Russian Agency for Patents and Trademarks
(ROSPATENT) added to list of core patent offices covered
NEWS 4 FEB 28 PATDPAFULL - New display fields provide for legal status
data from INPADOC
NEWS 5 FEB 28 BABS - Current-awareness alerts (SDIs) available
NEWS 6 FEB 28 MEDLINE/LMEDLINE reloaded
NEWS 7 MAR 02 GBFULL: New full-text patent database on STN
NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS 9 MAR 03 MEDLINE file segment of TOXCENTER reloaded
NEWS 10 MAR 22 KOREPAT now updated monthly; patent information enhanced
NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS 12 MAR 22 PATDPASPC - New patent database available
NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS 14 APR 04 EPFULL enhanced with additional patent information and new
fields.
NEWS 15 APR 04 EMBASE - Database reloaded and enhanced
NEWS 16 APR 18 New CAS Information Use Policies available online
NEWS 17 APR 25 Patent searching, including current-awareness alerts (SDIs),
based on application date in CA/CAPLUS and USPATFULL/USPAT2,
may be affected by a change in filing date for U.S.
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NEWS 18 APR 28 Improved searching of U.S. Patent Classifications for
U.S. patent records in CA/CAPLUS

NEWS EXPRESS JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

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FILE 'HOME' ENTERED AT 16:55:34 ON 29 APR 2005

=> file registry
COST IN U.S. DOLLARS

FULL ESTIMATED COST

| SINCE FILE
ENTRY | TOTAL
SESSION |
|---------------------|------------------|
| 0.21 | 0.21 |

FILE 'REGISTRY' ENTERED AT 16:56:02 ON 29 APR 2005
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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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```
=> s tgcttacat/sqen
      0 TGCTTACAT/SQEN
  107453 SQL=9
L1      0 TGCTTACAT/SQEN
        (TGCTTACAT/SQEN AND SQL=9)

=> s tgcttacat/sqsn
L2      201666 TGCTTACAT/SQSN

=> s l2 and SQL<400
    22713436 SQL<400
L3      14623 L2 AND SQL<400

=> file registry
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                                ENTRY          SESSION
                                39.81          40.02
FULL ESTIMATED COST
```

FILE 'REGISTRY' ENTERED AT 16:57:30 ON 29 APR 2005

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* available and contains the CA role and document type information. *
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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s 13
22713436 SQL<400
L4 14623 L2 AND SQL<400

=> s 14 and PY<1987
'1987' NOT A VALID FIELD CODE
0 PY<1987
L5 0 L4 AND PY<1987

=> file caplus
COST IN U.S. DOLLARS SINCE FILE TOTAL
ENTRY SESSION
5.03 45.05
FULL ESTIMATED COST

FILE 'CAPLUS' ENTERED AT 16:58:18 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate
substance identification.

=> s 13
L6 2668 L3

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=> s 16 and PY<1987
11536051 PY<1987
L7 . 4 L6 AND PY<1987

=> d bib ab hitseq 1-4

L7 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:536266 CAPLUS

DN 103:136266

TI Cotranscription of the large and small subunit genes of ribulose 1,5-bisphosphate carboxylase/oxygenase in Cyanophora paradoxa

AU Starnes, S. M.; Lambert, D. H.; Maxwell, E. S.; Stevens, S. E., Jr.; Porter, R. D.; Shively, J. M.

CS Dep. Biol. Sci., Clemson Univ., Clemson, SC, 29631, USA

SO FEMS Microbiology Letters (1985), 28(2), 165-9

CODEN: FMLED7; ISSN: 0378-1097

DT Journal

LA English

AB The region of the cyanelle genome of C. paradoxa which codes for ribulose-1,5-diphosphate carboxylase/oxygenase (I) [9027-23-0] was cloned and partially characterized. The large subunit gene (rbcL) is located adjacent to, and upstream from the small subunit gene (rbcS). The rbcS, contg. 318 nucleotides, codes for a polypeptide that exhibits greater homol. to small subunits of cyanobacteria than to those of angiosperms. Immediately downstream from the rbcS termination codon is an apparent transcription termination site consisting of an inverted repeat followed by a T cluster. The spacer region sepg. rbcL and rbcS is 105 nucleotides in length and lacks an obvious RNA polymerase promoter sequence suggesting that the genes are cotranscribed. Northern blot anal. has confirmed the cotranscription of both genes as a single transcript of ~2500 nucleotides.

IT 98443-94-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 98443-94-8 CAPLUS

CN DNA (Cyanophora paradoxa cyanelle gene rbcS) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgcaactta gaggagaacg taagttcgaa actttttctt atttaccacc
51 attaaacgcac caacagattt cgcgtcaatt acaatacgca ctttccaatg
101 gttatagccc agcaatcgaa ttcatgtttt caggtaaagc tgaagactta
151 gtatggactt tatggaaatt acctttattt ggtgcacaat ctccctgaaga
201 agtacttagc gaaattcaag cttgtaaaca acagttccct aatgcttaca
251 ttcgtgttgtt agcatttgac tctatcagac aagttcaaac ttatgttc
301 ttatgttaca aaccattata g

L7 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:417579 CAPLUS

DN 103:17579

TI Phage P22 lysis genes: nucleotide sequences and functional relationships with T4 and λ genes

AU Rennell, Dale; Poteete, Anthony R.

CS Med. Sch., Univ. Massachusetts, Worcester, MA, 01605, USA

SO Virology (1985), 143(1), 280-9

====

CODEN: VIRLAX; ISSN: 0042-6822

STN Columbus

DT Journal

LA English

AB Wild-type and amber mutant alleles of the lysis genes of phage P22 were cloned and sequenced. Gene 13 encodes an 11,520-dalton basic hydrophobic protein that has 89% amino acid homol. to λ S protein. Gene 19 encodes a protein that has a small degree of amino acid homol. with phage T4 lysozyme, but no homol. could be detected to λ R or RZ proteins. The protein product of gene 19 was purified; its N-terminal amino acid sequence is as predicted by the DNA sequence. It starts with a single N-terminal methionine residue and is a basic protein with a mol. wt. of 15,968. Plasmids expressing P22 gene 19, λ genes R and RZ, and T4 gene e were constructed. All of these plasmids were able to complement both λ R- and P22 19-.

IT 97047-61-5 97047-67-1

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 97047-61-5 CAPLUS

CN DNA (enterobacteria phage P22 gene 13) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaaaga tgccagaaaa acatgatctg ttaaccgcca tcatggcgcc
51 aaaggaacag ggcattcgaaa caatcctcgc gtttcaatg gcttaccttc
101 gcgttcggta taatggcggt gcgttaaga aaacactaat agacgcaacg
151 atgtgcgcca ttatcgctg gttcattcgt gaccttttag ttttcgcgg
201 actgagtagc aatcttgctt acatagcgag tttgtttatc ggctacatcg
251 gcacagactc gattgggtcg ctaatcaaac gtttcgctgc taaaaaaagcc
301 ggagtcgatg atgcaaatca gcagtaa

RN 97047-67-1 CAPLUS

CN DNA (enterobacteria phage P22 gene 13 mutant 13-h21) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaaaaaaga tgccagaaaa acatgatctg ttaaccgcca tcatggcgcc
51 aaaggaacag ggcattcgaaa caatcctcgc gtttcaatg gcttaccttc
101 gcgttcggta taatggcggt gcgttaaga aaacactaat agacgcaacg
151 atgtgcgcca ttatcgctg gttcattcgt gaccttttag ttttcgcgg
201 actgagtagc aatcttgctt acatagcgag tttgtttatc ggctacatcg
251 gcacagactc gattgggtcg ctaatcaaac gtttcgctgc taaaaaaagcc
301 ggagtcgatg atgcaaatca gcagtaa

L7 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:564673 CAPLUS

DN 101:164673

TI Tau, sigma, and delta. A family of repeated elements in yeast

AU Genbauffe, Francis S.; Chisholm, George E.; Cooper, Terrance G.

CS Dep. Biol. Sci., Univ. Pittsburgh, Pittsburgh, PA, 15260, USA

SO Journal of Biological Chemistry (1984), 259(16), 10518-25

====

CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB The isolation and structure of a new repeated DNA element, tau, is reported. This element, from *Saccharomyces cerevisiae*, is 371 base pairs

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(bp) long and is flanked on either end by the same invertedly repeated sequence found at the ends of some Ty and sigma elements in yeast, copia elements in Drosophila, and spleen necrosis virus. The tau inverted repeats are themselves flanked by a 5-bp directly repeated genomic sequence that is present only once in a cognate tau- allele. These structural characteristics, the presence of multiple copies of tau in the genome, and the isolation of tau+ and tau- allelic pairs suggest that tau may be capable of transposition either alone or in assocn. with some larger element. Detailed sequence anal. of the tau, sigma, and delta elements revealed that all 3 contain significant regions of homol., suggesting that they are probably members of a single family derived from a common progenitor.

IT 91756-05-7 92584-26-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 91756-05-7 CAPLUS

CN DNA (*Saccharomyces cerevisiae* clone pFG26 tau element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 tggtaaacg agagtaatta atagtgcacat gagttgttat ggttacaatt
51 caatgcctac atcgatatt aatgtacaaac tcgtatacgt ttaagtgtga
101 ttgcgcctat tgcagaagga atgttaaacg agaagctcag acaataactga
151 agctgtgtta aagacctatt agttgaacat gttatggtag gtacatatat
201 gaggaatatg agtcgtcaca tcaatgtata gtaactaccg gaatcactat
251 tatattggtc atgattaata tgaccaatcg gcgtgtgtt tatataccctc
301 tcttatttag tataagaaga tcagtaatta ttttttcatt aatactaatt
351 ttttacctct aattatcaac a

RN 92584-26-4 CAPLUS

CN DNA (*Saccharomyces cerevisiae* clone pGC106 tan element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 tggtaaacg agagtaatta atagtgcacat gagttgttat ggttacaatc
51 taatgcctac atcgatatt aatgtacacc tcgtatacgt ttaagtgtga
101 ttgcgcctat tgcagaagga atgttaaacg agaagctcag acaataactga
151 agctgtgtta aacacctatt agttgaacat gttatggtag gtacatatat
201 gaggaatatg agtcgtcaca tcaatgtata gtaactaccg gaatcactat
251 tatattggtc atgattaata tgaccaatcg gcgtgtgtt tatataccctc
301 tcttatttag tataagaaga tcagtaatta ttttttcatt aatactaattt
351 ttttacctct aattatcaac a

L7 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:505082 CAPLUS

DN 101:105082

TI tau, A repeated DNA sequence in yeast

AU Chisholm, George E.; Genbauffe, Francis S.; Cooper, Terrance G.

CS Dep. Biol. Sci., Univ. Pittsburgh, Pittsburgh, PA, 15260, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1984), 81(10), 2965-9

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

STN Columbus

LA English
 AB A 371-base-pair (bp) repeated DNA element, tau, was found in *Saccharomyces cerevisiae*. The ends of tau are composed of a 5-bp inverted repeat, similar in sequence to those reported for the Ty, sigma, copia, and spleen necrosis virus elements. These inverted repeats are flanked by 5-bp direct repeats of a target sequence that occurs only once in an allele that lacks the tau element. This overall structure is characteristic of transposable elements. Like sigma, tau elements were found (in both orientations) closely assocd. with tRNA genes (409 and 198 bp from the 5' end, resp.). It is noteworthy that 1 representative of tau was isolated in a concentric insertion of tau, delta, and sigma.

IT 91756-05-7

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 91756-05-7 CAPLUS

CN DNA (*Saccharomyces cerevisiae* clone pFG26 tau element) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 tggtaaacg agagtaatta atagtgacat gagttgtat ggttacaatt
 51 caatgcctac atcgatatatt aatgtacaac tcgtatacgt ttaagtgtga
 101 ttgcgcctat tgccagaagga atgttaaacg agaagcttag acaatactga
 151 agctgttta aagaccattt agttgaacat gttatggtag gtacatataat
 201 gagaaatatg agtcgtcaca tcaatgtata gtaactaccg gaatcactat
 251 tatattggtc atgattaata tgaccaatcg gcgtgtttt tatataccctc
 301 tcttatttag tataagaaga tcagtaatta tttcttcatt aatactaatt
 351 tttaacctct aattatcaac a

=> file stnguide

COST IN U.S. DOLLARS

| | SINCE FILE ENTRY | TOTAL SESSION |
|---------------------|------------------|---------------|
| FULL ESTIMATED COST | 33.69 | 78.74 |

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

| | SINCE FILE ENTRY | TOTAL SESSION |
|---------------------|------------------|---------------|
| CA SUBSCRIBER PRICE | -2.92 | -2.92 |

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=> file registry

COST IN U.S. DOLLARS

| | SINCE FILE ENTRY | TOTAL SESSION |
|---------------------|------------------|---------------|
| FULL ESTIMATED COST | 0.30 | 79.04 |

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

| | SINCE FILE ENTRY | TOTAL SESSION |
|---------------------|------------------|---------------|
| CA SUBSCRIBER PRICE | 0.00 | -2.92 |

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```
=> s cactcatat/sqen
      0 CACTCATAT/SQEN
      107453 SQL=9
L8      0 CACTCATAT/SQEN
      (CACTCATAT/SQEN AND SQL=9)

=> s cactcatat/sqsn
L9      157456 CACTCATAT/SQSN

=> s l9 and SQL<400
      22713436 SQL<400
L10     9780 L9 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                                ENTRY        SESSION
FULL ESTIMATED COST          39.81           118.85

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE      TOTAL
                                                ENTRY        SESSION
CA SUBSCRIBER PRICE           0.00            -2.92
```

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=> s l10
L11 2154 L10

=> s l11 and PY<1987
11536051 PY<1987
L12 1 L11 AND PY<1987

=> d bib ab hitseq

L12 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:29657 CAPLUS

DN 104:29657

TI Burkitt lymphoma cell line carrying a variant translocation creates new DNA at the breakpoint and violates the hierarchy of immunoglobulin gene rearrangement

AU Denny, Christopher T.; Hollis, Gregory F.; Magrath, Ian T.; Kirsch, Ilan R.

CS Navy Med. Oncol. Branch, Natl. Cancer Inst., Bethesda, MD, 20205, USA

SO Molecular and Cellular Biology (1985), 5(11), 3199-207

CODEN: MCEBD4; ISSN: 0270-7306

DT Journal

LA English

AB The Burkitt lymphoma cell line KK124, which contains a reciprocal t(8;22) translocation, rearranged in a region 3' to the c-myc proto-oncogene on chromosome 8 and 5' to the λ const. region on chromosome 22. The breakpoint was cloned and sequenced, revealing the c-myc and a portion of its 3' region abutted a complete λ variable gene that had undergone V-J recombination. Since this cell line expresses κ light chain, this λ rearrangement violates the previously proposed hierarchy of Ig gene rearrangement. A novel duplication of normal chromosome 8 sequences was also found at the breakpoint. The 1st exon of c-myc and its flanking sequence from the translocated allele was sequenced and compared with a normal counterpart. Extensive mutation was found within the 1st exon, in contrast to its 3'- and 5'-flanking regions. S1 nuclease anal. revealed that the translocated c-myc was expressed and that there was a promoter shift from P2 to P1. The detailed structural anal. of this cell line provides clues concerning mechanisms of chromosomal translocation and c-myc deregulation in Burkitt lymphomas.

IT 99752-03-1

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 99752-03-1 CAPLUS

CN DNA (human Burkitt's lymphoma KK124 immunoglobulin Vλ gene) (9CI)
(CA INDEX NAME)

NTE doublestranded

STN Columbus

SEQ 1 tctgccctga ctcagcctgc ctccgtgtct gggctcctg gacagtgcat
51 caccatctcc tgcattggaa tcaacagtga catttgcgt tgtaactatg
101 tctccggta ccaacagcac ccagccaaag ccccccaaact catgatttat
151 gaggtcaaga atccggccctc agggtttct aatcgcttct ctggctccaa
201 gtctgccaac acggcctccc tgaccatctc tgggctccag gctgaggacg
251 aggctgatta ttactacact catatacaga caccagcact ctcgggtg

| | | | |
|--|------------------|---------------|--|
| => file registry | | | |
| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION | |
| FULL ESTIMATED COST | 11.64 | 130.49 | |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION | |
| CA SUBSCRIBER PRICE | -0.73 | -3.65 | |

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* available and contains the CA role and document type information. *
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Crossover limits have been increased. See HELP CROSSOVER for details.

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information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s gaaggtcct/sqen
0 GAAGGTCC/T/SQEN
107453 SQL=9
L13 0 GAAGGTCC/T/SQEN
(GAAGGTCC/T/SQEN AND SQL=9)

=> s gaaggtcct/sqsn

STN Columbus

L14 193989 GAAGGTCC/SQSN

=> s l14 and SQL<400
22713436 SQL<400
L15 16920 L14 AND SQL<400

| | | |
|--|------------------|---------------|
| => file caplus | SINCE FILE ENTRY | TOTAL SESSION |
| COST IN U.S. DOLLARS | 39.81 | 170.30 |
| FULL ESTIMATED COST | | |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -3.65 |

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s l15
L16 2703 L15

=> s l16 and PY<1987
11536051 PY<1987
L17 4 L16 AND PY<1987

=> d bib ab hitseq 1-4

L17 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:83077 CAPLUS
DN 104:83077
TI Genetic expression of somatostatin as hybrid polypeptide
IN Canosi, Umberto; De Fazio, Gabriele; Villa, Stefano; Donini, Silvia
PA Istituto Farmacologico Serono S.p.A., Italy
SO Eur. Pat. Appl., 21 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------|-------|-------|-----------------|-------|
| ----- | ----- | ----- | ----- | ----- |

STN Columbus

| | | | | | | |
|------|---|--------|-----------------|----------------|--------------|--|
| PI | EP 160190 | A2 | 19851106 | EP 1985-102891 | 19850313 <-- | |
| | EP 160190 | A3 | 19870715 | | | |
| | R: AT, CH, DE, FR, GB, LI, NL, SE | | | | | |
| | IL 74620 | A1 | 19901223 | IL 1985-74620 | 19850315 | |
| | ZA 8502035 | A | 19851127 | ZA 1985-2035 | 19850319 <-- | |
| | DK 8501312 | A | 19851001 | DK 1985-1312 | 19850322 <-- | |
| | AU 8540461 | A1 | 19851031 | AU 1985-40461 | 19850328 <-- | |
| | FI 8501288 | A | 19851001 | FI 1985-1288 | 19850329 <-- | |
| | NO 8501308 | A | 19851001 | NO 1985-1308 | 19850329 <-- | |
| | ES 541782 | A1 | 19860401 | ES 1985-541782 | 19850329 | |
| | CA 1301676 | A1 | 19920526 | CA 1985-477979 | 19850329 | |
| | JP 61005788 | A2 | 19860111 | JP 1985-65088 | 19850330 <-- | |
| | US 5268278 | A | 19931207 | US 1988-193202 | 19880509 | |
| | AU 8939547 | A1 | 19891130 | AU 1989-39547 | 19890811 | |
| | AU 611048 | B2 | 19910530 | | | |
| PRAI | IT 1984-47976 | A | 19840330 | | | |
| | US 1985-717444 | B1 | 19850329 | | | |
| AB | Recombinant plasmid vectors are described that contain the entire Trp regulatory system (promoter, operator, leader, and attenuator) and a synthetic gene that encodes somatostatin. Thus a plasmid, pSP3, was constructed that contained the Trp regulatory region, the 1st 323 codons of the TrpE gene, and a linker sequence. A synthetic gene for somatostatin was prep'd. and inserted into the linker region of pSP3 to yield pSP4. Plasmid pSP4 encoded a fusion protein comprised of 323 amino acids of the TrpE protein, 4 amino acids encoded by the linker region, and somatostatin. The somatostatin was released from the fusion protein by CNBr treatment. The yield was ~300 µg somatostatin/L of Escherichia coli culture. The yield was increased to 400 µg/L if indole was used instead of tryptophan to derepress the tryptophan operon. | | | | | |
| IT | 100438-83-3 | | | | | |
| | RL: PRP (Properties); BIOL (Biological study) | | | | | |
| | (nucleotide sequence of) | | | | | |
| RN | 100438-83-3 | CAPLUS | | | | |
| CN | DNA, (sheep somatostatin[Met-1]-specifying) | (9CI) | (CA INDEX NAME) | | | |
| NTE | doublestranded (2) | | | | | |
| SEQ | 1 agcttacatg gccggttgca agaacttctt ctggaagacc ttcacctctt
51 gctag

1 gatccttagca agaggtgaag gtcctccaga agaagttctt gcaaccggcc
51 atgta | | | | | |

L17 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:573361 CAPLUS
 DN 103:173361
 TI Cloning and expression of the 1.3 S biotin-containing subunit of transcarboxylase
 AU Murtif, Vicki L.; Bahler, Chris R.; Samols, David
 CS Dep. Biochem., Case Western Reserve Univ., Cleveland, OH, 44106, USA
 SO Proceedings of the National Academy of Sciences of the United States of America (1985), 82(17), 5617-21
 =====
 CODEN: PNASA6; ISSN: 0027-8424
 DT Journal
 LA English
 AB The gene coding for the 1.3 S biotin-contg. subunit of transcarboxylase (EC 2.1.3.1) [9029-86-1] from Propionibacterium shermanii was cloned.

STN Columbus

Transcarboxylase is a well-characterized enzyme composed of 30 polypeptides of 3 different types; 12 1.3 S biotinyl subunits, 6 5 S dimeric outer subunits, and 1 12 S hexameric central subunit. In propionic acid fermn., the enzyme catalyzes the transfer of a carboxyl group from methylmalonyl-CoA to pyruvate in 2 partial reactions. The 1.3 S subunit binds the outer and central subunits of the enzyme together, and its biotin serves as carboxyl carrier between subsites on the central and outer subunits where each partial reaction occurs. The cloned gene was expressed in Escherichia coli, and the 1.3 S subunit accumulates to 7% of total cellular protein. The foreign protein is recognized and biotinated by biotin holoenzyme synthetase of E. coli. The identifications of the gene and its product were confirmed by 4 independent approaches; DNA sequence anal., immunopptn., incorporation of labeled biotin, and measurement of enzymic activity in the 1st partial reaction.

IT 98824-75-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 98824-75-0 CAPLUS

CN DNA (Propionibacterium shermanii methylmalonyl coenzyme A carboxyltransferase biotinyl subunit gene) (9CI) (CA INDEX NAME)

SEQ 1 atgaaaactga aggttaacagt caacggca ctgcgtatgacg ttgacgttga
51 cgtcgacaag tcacacgaaa acccgatggg caccatcctg ttcggccggcg
101 gcaccggcg cgccggca ccgcgcgcag cagggtggcgc aggccgggt
151 aaggccggag agggcgagat tcccgcgtccg ctggccggca ccgtctccaa
201 gatcctcgatg aaggagggtg acacggtcaa ggctgttcag accgtgcgtc
251 ttctcgaggc catgaagatg gagaccgaga tcaacgctcc caccgacggc
301 aaggtcgaga aggtccttgtt caaggagcgt gacgcgtgc agggcggtca
351 gggtctcatc aagatcggtc ga

I.17 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:90720 CAPLUS

DN 102:90720

TI Molecular cloning and nucleotide sequence of a variant wheat histone H4 gene

AU Täbata, Tetsuya; Iwabuchi, Masaki
CS Fac. Sci., Hokkaido Univ., Sapporo, 060, Japan

SO Gene (1984), 31(1-3), 285-9

====

CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB To det. whether there is structural variation among histone H4 genes in wheat, one (TH091) of the H4 genes that had been cloned from a wheat genomic DNA library was sequenced and compared with another H4 gene (TH011) described previously. There are 17 nucleotide replacements in the protein-coding region of 2 H4 genes, causing only 1 amino acid substitution: a glycine at position 4 (from the N terminus) in TH011 was replaced by an aspartic acid in TH091. S1 mapping, using total nuclear RNA from germinated seeds, indicated that the H4 gene was transcribed in vivo.

IT 94895-12-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 94895-12-2 CAPLUS

CN DNA (wheat clone pTH091 histone H 4 gene) (9CI) (CA INDEX NAME)

STN Columbus

NTE doublestranded

SEQ 1 atgtctggc gcgacaaggg cggcaagggg ctggcaagg gcccgccaa
 51 gccgcaccgg aaggcttcc gcgacaacat ccagggcatc accaagccgg
 101 cgatccggag gctggccagg aggggcggcg tgaagcgcat ctccggcctc
 151 atctacgagg agacccggcg cgtcctcaag atcttcctcg agaacgtcat
 201 cccgcacgcc gtcacctaca ccgagcacgc ccgcccggaaa accgtcaccg
 251 ccatggacgt cgtctacgct ctcaagcgcc agggccgcac cctctacggc
 301 ttccggaggct ag

L17 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:607278 CAPLUS

DN 99:207278

TI The structural organization and DNA sequence of a wheat histone H4 gene

AU Tabata, Tetsuya; Sasaki, Kimiko; Iwabuchi, Masaki

CS Fac. Sci., Hokkaido Univ., Sapporo, 060, Japan

SO Nucleic Acids Research (1983), 11(17), 5865-75

====

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB Wheat histone H4 genes were cloned from a Charon 4 wheat genomic DNA library, using sea urchin histone H4 DNA as a probe. DNA sequence anal. of a cloned gene showed that the deduced amino acid sequence of wheat histone H4 protein was identical to that of pea. The 5' end of wheat histone H4 mRNA was mapped on the cloned gene by the S1 procedure. Southern blot anal. of the genomic DNA indicated that histone H4 genes were reiterated 100-125 times/hexaploid wheat genome.

IT 87915-36-4

RL: PRP (Properties); BIOL (Biological study)
 (nucleotide sequence of)

RN 87915-36-4 CAPLUS

CN DNA (wheat clone pTH011 histone H4 gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgtccggc gcggcaaggg aggcaaggc ctaggcaagg gcccgccaa
 51 .gcgcaccgg aaggcttcc gcgataacat ccagggcatc accaagccgg
 101 cgatccggcg gctggccgg cggggcggcg tgaagcgcat ctccggcctc
 151 atctacgagg agacccggcg cgtcctcaag atcttcctcg agaacgtcat
 201 cccgcatgcc gtacactaca ccgagcacgc ccgcccggaa accgtcaccg
 251 ccatggacgt cgtctacgct ctcaagcgcc agggccgcacc ctctacggct
 301 tcggcggcta a

=> file registry

COST IN U.S. DOLLARS

| SINCE FILE
ENTRY | TOTAL
SESSION |
|---------------------|------------------|
| 34.59 | 204.89 |

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

| SINCE FILE
ENTRY | TOTAL
SESSION |
|---------------------|------------------|
| -2.92 | -6.57 |

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s gggagtacg/sqen
      0 GGGAGTACG/SQEN
      107453 SQL=9
L18      0 GGGAGTACG/SQEN
          (GGGAGTACG/SQEN AND SQL=9)

=> s gggagtacg/sqsn
L19      116522 GGGAGTACG/SQSN

=> s l19 and SQL<400
      22713436 SQL<400
L20      5701 L19 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS           SINCE FILE TOTAL
                                ENTRY SESSION
FULL ESTIMATED COST           39.81    244.70

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE TOTAL
                                              ENTRY SESSION
CA SUBSCRIBER PRICE            0.00     -6.57
```

FILE 'CAPLUS' ENTERED AT 17:13:47 ON 29 APR 2005
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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s l20
L21 1154 L20

=> s l21 and PY<1987
11536051 PY<1987
L22 0 L21 AND PY<1987

=> s l21 and PY<1988
12016813 PY<1988
L23 0 L21 AND PY<1988

| | SINCE FILE ENTRY | TOTAL SESSION |
|--|------------------|---------------|
| COST IN U.S. DOLLARS | 4.23 | 248.93 |
| FULL ESTIMATED COST | | |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -6.57 |

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s ggtatttga/sqen
      0 GGTATTG/A/SQEN
      107453 SQL=9
L24          0 GGTATTG/A/SQEN
              (GGTATTG/A/SQEN AND SQL=9)
```

```
=> s ggtatttga/sqsn
L25          182237 CGTATTG/A/SQSN
```

```
=> s l25 and SQL<400
      22713436 SQL<400
L26          12680 L25 AND SQL<400
```

| | SINCE FILE
ENTRY | TOTAL
SESSION |
|--|---------------------|------------------|
| COST IN U.S. DOLLARS | | |
| FULL ESTIMATED COST | 39.81 | 288.74 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE
ENTRY | TOTAL
SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -6.57 |

FILE 'CAPLUS' ENTERED AT 17:15:34 ON 29 APR 2005
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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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```
=> s l26
L27          2552 L26

=> s l27 and PY<1987
      11536051 PY<1987
L28          1 L27 AND PY<1987
```

STN Columbus

=> d bib ab hitseq

L28 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:13879 CAPLUS

DN 106:13879

TI Different human cervical carcinoma cell lines show similar transcription patterns of human papillomavirus type 18 early genes

AU Schneider-Gaedicke, Ansbert; Schwarz, Elisabeth

CS Inst. Virusforsch., Dtsch. Krebsforschungszent., Heidelberg, 6900, Fed. Rep. Ger.

SO EMBO Journal (1986), 5(9), 2285-92

CODEN: EMJODG; ISSN: 0261-4189

DT Journal

LA English

AB Transcription of human papillomavirus type 18 (HPV18) DNA in the human cervical carcinoma cell lines HeLa, C4-1 and SW756 was studied by nucleotide sequence anal. of HPV18-pos. cDNA clones isolated from a HeLa, C4-1 and SW756 cDNA library, resp., and the cDNA sequences were used to predict the potential encoded proteins. The cDNA clones from all 3 cell lines were found to be derived from virus-cell fusion transcripts in which 3'-terminal host cell sequences (different for each cell line) were spliced to 5'-terminal exon sequences from the HPV18 E6-E7-E1 region. Three different types of cDNA clones can be distinguished according to the splicing patterns obsd. in the 5' terminal HPV18 sequences. They carry as potential protein-coding regions the HPV18 specific open reading frames E6 and E6* (generated by splicing and identical with E6 up to the E6* splice junction), E7 and E1 (only in HeLa). Translation of specific cellular genes from the chimeric viral-cellular transcripts seem to be unlikely. The mapping of the 5'-ends of the virus-cell fusion transcripts indicates that transcription is initiated at a viral promoter. The similar patterns of HPV18 transcription in the 3 different cervical carcinoma cell lines suggest a functional role of HPV18 early genes for the malignant phenotype of these cells.

IT 105843-47-8

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 105843-47-8 CAPLUS

CN DNA (human papillomavirus 18 protein E 6* cDNA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggcgcgct ttgaggatcc aacacggcga ccctacaagc tacctgatct
51 gtgcacggaa ctgagcaatt cactgcaaga catagaata acctgttat
101 attgcaagac agtattggaa cttacagagg tatttgaatt tgcatataaa
151 gatttatgg tggtgatag agacagtata ccgcattgtg catgccataa
201 atgtatacat ttttattcta gaatttagaga attaagacat tattcagact
251 ctgtgtatgg agacacattg gaaaaactaa ctaacactgg gttatacat
301 ttattaataa ggtgcctgcg gtgccagaaa ccgttgaatc cagcagaaaa
351 accttag

=> file registry

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY SESSION

FULL ESTIMATED COST

10.74 299.48

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

SINCE FILE

TOTAL

STN Columbus

| | ENTRY | SESSION |
|---------------------|-------|---------|
| CA SUBSCRIBER PRICE | -0.73 | -7.30 |

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s caaggggcc/sqen
      0 CAAGGGGCC/SQEN
  107453 SQL=9
L29      0 CAAGGGGCC/SQEN
          (CAAGGGGCC/SQEN AND SQL=9)

=> s caaggggcc/sqsn
L30      155151 CAAGGGGCC/SQSN

=> s l30 and SQL<400
      22713436 SQL<400
L31      13136 L30 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS          SINCE FILE    TOTAL
                                ENTRY        SESSION
FULL ESTIMATED COST          39.81         339.29

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE    TOTAL
                                                ENTRY        SESSION
CA SUBSCRIBER PRICE           0.00          -7.30
```

FILE 'CAPLUS' ENTERED AT 17:18:38 ON 29 APR 2005
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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s l31
L32 2424 L31

=> s l32 and PY<1987
11536051 PY<1987
L33 1 L32 AND PY<1987

=> d bib ab hitseq

L33 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:124233 CAPLUS
DN 104:124233
TI Plasmid carrying sequences encoding salmon pituitary hormones or their precursors
IN Soma, Genichiro; Kitahara, Namiko; Okazaki, Hideo
PA Seikagaku Kogyo Co., Ltd., Japan
SO Jpn: Kokai Tokkyo Koho, 9 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--------------------|------|----------|-----------------|-------------|
| PI JP 60176588 | A2 | 19850910 | JP 1984-32700 | 19840224 <- |
| PRAI JP 1984-32700 | | 19840224 | | |

AB Plasmids carrying base sequences encoding salmon pituitary hormones or their precursors are constructed. Base sequences that encode proopiomelanocorticotropin, corticotropin, α -melanotropin, corticotropin-like peptide, β -lipotropin, α -lipotropin, β -melanotropin, β -endorphin and salmon gonadotropin are given. Thus, mRNA isolated from the pituitary gland of salmon was used in the prepn. of cDNAs which were inserted into the PstI site of plasmid pBR322 for the transformation of Escherichia coli. Construction of plasmid pSSM17 (for transformation of E. coli for the prodn. of salmon precorticotropin) is given as an example.

IT 100984-20-1 100984-21-2
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 100984-20-1 CAPLUS
CN DNA, d(C-A-G-C-T-G-G-C-A-G-C-T-G-G-A-G-G-A-C-G-A-G-A-T-G-G-T-G-G-A-G-

STN Columbus

C-T-C-T-G-G-G-A-A-C-C-A-A-G-G-G-C-C-A-A-G-G-C-T-C-A-G-A-C-C-A-A-G-G-T-A-G-T-C-C-C-A-G-A-C-C-C-T-C-A-C-T-G-T-G-A-C-G-G-G-C-T-G-C-A-A-G-A-T-A-A-G-A-A-G-G-A-T-G-G-G-T-C-C-T-A-T-C-G-G-A-T-G-G-G-T-C-A-C-T-T-C-C-G-C-T-G-G-G-C-A-G-C-C-C-A-A-C-C-G-C-T-A-T-C-A-A-G-C-G-C-T-A-C-G-G-T-G-G-C-T-T-G-C-A-T-G-A-A-G-C-C-A-T-A-C-C-A-A-G-C-A-A-T-C-C-C-A-C-A-A-G-C-C-C-T-G-C-A-T-C-A-C-G-C-T-G-C-T-C-A-A-G-C-A-G-C-A-G-C-C-T-G-A-G) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 cagctggca gctgggagga cgagatggtg ggagctctgg ggaaccaagg
 51 ggc当地ggct cagaccaagg tagtccccag aaccctcaact gtgacggggc
 101 tgcaagataa gaaggatggg tcctatcgga tgggtcaatt cc当地ctggggc
 151 agcccaaccg ctatcaagcg ctacggggc ttcatgaagc catataccaa
 201 gcaatcccac aagccctga. tcaacgctgct caagcacatc acccttaaga
 251 acgagcag

RN 100984-21-2 CAPLUS

CN DNA, d(C-A-G-C-T-G-G-G-C-A-G-C-T-G-G-G-A-G-G-A-C-G-A-T-G-G-G-A-G-C-T-C-T-G-G-G-G-A-A-C-C-A-A-G-G-G-C-C-A-A-G-G-C-T-C-A-G-A-C-C-A-A-G-G-T-A-G-T-C-C-C-C-A-G-A-A-C-C-C-T-C-A-C-T-G-T-G-A-C-G-G-G-G-C-T-G-C-A-A-G-A-T-A-A-G-A-A-G-G-A-T-G-G-T-C-C-T-A-T-C-G-G-A-T-G-G-G-T-C-A-C-T-T-C-C-G-C-T-A-A-G-A-A-G-C-C-A-C-C-T-A-T-C) (9CI) (CA INDEX NAME)

NTE singlestranded

SEQ 1 cagctggca gctgggagga cgagatggtg ggagctctgg ggaaccaagg
 51 ggc当地ggct cagaccaagg tagtccccag aaccctcaact gtgacggggc
 101 tgcaagataa gaaggatggg tcctatcgga tgggtcaatt cc当地ctggggc
 151 agcccaaccg ctatc

=> file registry
 COST IN U.S. DOLLARS

| SINCE FILE ENTRY | TOTAL SESSION |
|------------------|---------------|
| 10.74 | 350.03 |

FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

| SINCE FILE ENTRY | TOTAL SESSION |
|------------------|---------------|
| -0.73 | -8.03 |

CA SUBSCRIBER PRICE

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```
*****
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added,      *
* effective March 20, 2005. A new display format, IDERL, is now        *
* available and contains the CA role and document type information.   *
*****
```

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s acggcaagg/sqen
      0 ACGGCAAGG/SQEN
  107453 SQL=9
L34      0 ACGGCAAGG/SQEN
          (ACGGCAAGG/SQEN AND SQL=9)

=> s acggcaagg/sqsn
L35      140454 ACGGCAAGG/SQSN

=> s l35 and SQL<400
      22713436 SQL<400
L36      12155 L35 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS           SINCE FILE      TOTAL
                                ENTRY       SESSION
FULL ESTIMATED COST           39.81        389.84

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE      TOTAL
                                              ENTRY       SESSION
CA SUBSCRIBER PRICE            0.00         -8.03
```

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substance identification.

=> s 136
L37 2202 L36

=> s 137 and PY<1987\
NUMERIC VALUE NOT VALID '1987\'
Numeric values may contain 1-8 significant figures. If range notation
is used, both the beginning and the end of the range must be
specified, e.g., '250-300/MW'. Expressions such as '250-/MW' are not
allowed. To search for values above or below a given number, use the
>, =>, <, or <= operators, e.g., 'MW => 250'. Text terms cannot be
used in numeric expressions. If you specify a unit, it must be
dimensionally correct for that field code. To see the unit
designations for field codes in the current file, enter "DISPLAY UNIT
ALL" at an arrow prompt (=>).

=>
* * * * * RECONNECTED TO STN INTERNATIONAL * * * * *
SESSION RESUMED IN FILE 'CAPLUS' AT 17:22:26 ON 29 APR 2005
FILE 'CAPLUS' ENTERED AT 17:22:26 ON 29 APR 2005

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| | SINCE FILE
ENTRY | TOTAL
SESSION |
|--|---------------------|------------------|
| COST IN U.S. DOLLARS | | |
| FULL ESTIMATED COST | 0.45 | 390.29 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE
ENTRY | TOTAL
SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -8.03 |

=> s 137 and PY<1987
11536051 PY<1987
L38 3 L37 AND PY<1987

=> d bib ab hitseq 1-3

L38 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:528776 CAPLUS
 DN 105:128776
 TI Cloning and sequencing of the gene encoding cytochrome c3 from
Desulfovibrio vulgaris (Hildenborough)
 AU Voordouw, Gerrit; Brenner, Sydney
 CS Dep. Biochem., Agric. Univ. Wageningen, Wageningen, NL-6703 BC, Neth.
 SO European Journal of Biochemistry (1986), 159(2), 347-51
 CODEN: EJBCAI; ISSN: 0014-2956
 DT Journal
 LA English
 AB The gene encoding the redox protein cytochrome c3 [9035-44-3] from *D. vulgaris* (Hildenborough) was cloned using 2 synthetic oligonucleotides (one 17-mer and one 18-mer), designed to recognize the structural gene. Plasmid pCYC3 was derived from the clone and contains a 7.5 x 103-base EcoRI-HindIII insert of *D. vulgaris* DNA in pUC9. A 674-base-pair fragment of this insert was sequenced with the dideoxy-chain-termination procedure and found to contain the entire structural gene encoding cytochrome c3 bracketed by apparent *Escherichia coli* consensus for initiation and termination of transcription. The amino acid sequence of 107 residues, derived from protein sequencing, is confirmed by the nucleic acid sequence, which shows in addn. that it is preceded by a hydrophobic, pos. charged signal sequence of 21 residues. This N-terminal extension functions in the export of cytochrome c3, which is thought to reside in the periplasm of *D. vulgaris*.

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IT 104219-92-3

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 104219-92-3 CAPLUS

CN DNA (Desulfovibrio vulgaris clone pCYC3 cytochrome c3 gene) (9CI) (CA
INDEX NAME)

NTE doublestranded

SEQ 1 atgaggaaac tggtttctg cgccgtactc gcccggccg tagcccttgc
51 gtcggcggtt gtggccgctc ccaaggcccc tggccgacggc ctgaagatgg
101 aagccaccaa gcagccccgtg gtttcaacc actccaccca caagtccgtg
151 aagtgtgggt actgcccacca ccccgtaaac ggcaaggaaag actaccgcaa
201 gtgcgggtacc gcccgtgcc acgacagcat ggacaagaag gacaagtccg
251 cgaaggggcta ctatcatgtc atgcatgaca agaacaccaa gttcaagtcc
301 tgcgtgggtt gccacgttga agtggccgtt gccgatggcc ccaagaagaa
351 ggacctcacc ggctgcaaga agtccaagtg ccacgaataag

L38 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:573361 CAPLUS

DN 103:173361

TI Cloning and expression of the 1.3 S biotin-containing subunit of
transcarboxylase

AU Murtif, Vicki L.; Bahler, Chris R.; Samols, David

CS Dep. Biochem., Case Western Reserve Univ., Cleveland, OH, 44106, USA

SO Proceedings of the National Academy of Sciences of the United States of
America (1985), 82(17), 5617-21

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The gene coding for the 1.3 S biotin-contg. subunit of transcarboxylase
(EC 2.1.3.1) [9029-86-1] from Propionibacterium shermanii was cloned.
Transcarboxylase is a well-characterized enzyme composed of 30
polypeptides of 3 different types; 12 1.3 S biotinyl subunits, 6 5 S
dimeric outer subunits, and 1 12 S hexameric central subunit. In
propionic acid fermn., the enzyme catalyzes the transfer of a carboxyl
group from methylmalonyl-CoA to pyruvate in 2 partial reactions. The 1.3
S subunit binds the outer and central subunits of the enzyme together, and
its biotin serves as carboxyl carrier between subsites on the central and
outer subunits where each partial reaction occurs. The cloned gene was
expressed in Escherichia coli, and the 1.3 S subunit accumulates to 7% of
total cellular protein. The foreign prtein is recognized and biotinated
by biotin holoenzyme synthetase of E. coli. The identifications of the
gene and its product were confirmed by 4 independent approaches; DNA
sequence anal., immunopptn., incorporation of labeled biotin, and
measurement of enzymic activity in the 1st partial reaction.

IT 98824-75-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 98824-75-0 CAPLUS

CN DNA (Propionibacterium shermanii methylmalonyl coenzyme A
carboxyltransferase biotinyl subunit gene) (9CI) (CA INDEX NAME)

SEQ 1 atgaaaactga aggttaacagt caacggcact gcgtatgacg ttgacgttga
51 cgtcgacaag tcacacgaaa acccgatggg caccatctg ttccggggcg
101 gcaccggcg cgcgcggca cgcgcgcag caggtggcgc aggccgggt

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```

151 aaggccggag agggcgagat tcccgtccg ctggccggca ccgtctccaa
201 gatcctcgta aaggagggtg acacggtaa ggctggtcag accgtgtcg
251 ttctcgaggc catgaagatg gagaccgaga tcaacgtcc caccgacggc
301 aaggtcgaga aggtccttgtt caaggagcgt gacgccgtgc agggcggtca
351 gggtctcatc aagatcggtc ga

```

L38 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1981:187080 CAPLUS

DN 94:187080

TI The nucleotide sequence of the hepatitis B viral genome and the identification of the major viral genes

AU Valenzuela, Pablo; Quiroga, Margarita; Zaldivar, Josefina; Gray, Patrick; Rutter, William J.

CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA

SO ICN-UCLA Symposia on Molecular Cellular Biology (1980), 18(Anim. Virus

====

Genet.), 57-70

CODEN: IUSMDJ; ISSN: 0097-9023

DT Journal

LA English

AB The complete sequence (3221 nucleotides) of the hepatitis B viral DNA (adw2 serotype) is reported. The long strand has 4 major polypeptide coding regions with an aggregate translational capacity of 1613 amino acids (4839 nucleotides). Two genes coding for the major viral proteins were identified: the previously described surface antigen gene coding for a protein of 25,398 daltons, and the core antigen gene, which codes for a basic polypeptide (21,335 daltons) with a striking protamine-like sequence at its C-terminus. There are 3 other putative peptide coding regions: a, which overlaps the surface antigen gene and may code for a protein up to ~95,000 daltons and B, which partially overlaps the core gene and may code for a peptide of ~16,000 daltons. The short strand of the virus is largely devoid of possible peptide coding regions. A single segment capable of coding a peptide of 94 amino acids is identified.

IT 77271-73-9

RL: PRP (Properties)

(nucleotide sequence of)

RN 77271-73-9 CAPLUS

CN DNA (hepatitis B virus subtype adw2 clone pEco-3/pEco-63/pPst-7 protein D gene) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ:

| | |
|-----|--|
| 1 | atgtagccttg actgttaaga cagcaggaga gcgcctttat atgttagcaaa |
| 51 | ggtaccgcac atccgacatg acgggtgacc taggaagcgc cctgcaggaa |
| 101 | acaaaatgcag ggcagccgcg acttagggcg cctgctgggg agagccccgg |
| 151 | cgaaccctga gagagcaggg yaagaggcag acggcaaggt cgctgggtgc |
| 201 | cccgcggtga gagaatgcg ccagaggggc agacacggaa gatgtacgg |
| 251 | ccaggcacac gtgaagcgaa gtggagacgt gcaacgta |

=> file registry
COST IN U.S. DOLLARS
FULL ESTIMATED COST

| SINCE FILE | TOTAL |
|------------|---------|
| ENTRY | SESSION |
| 27.09 | 416.93 |

STN Columbus

| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
|--|------------------|---------------|
| CA SUBSCRIBER PRICE | -2.19 | -10.22 |

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DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s cgtacatcg/sqen
      0 CGTACATCG/SQEN
      107453 SQL=9
L39      0 CGTACATCG/SQEN
          (CGTACATCG/SQEN AND SQL=9)

=> s cgtacatcg/sqsn
L40      36728 CGTACATCG/SQSN

=> s l40 and SQL<400
      22713436 SQL<400
L41      4611 L40 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS           SINCE FILE ENTRY   TOTAL SESSION
                                39.81        456.74
FULL ESTIMATED COST

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE ENTRY   TOTAL SESSION
                                                0.00        -10.22
CA SUBSCRIBER PRICE
```

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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s 141
L42 769 L41

=> s 142 and PY<1987
11536051 PY<1987
L43 2 L42 AND PY<1987

=> d bib ab hitseq 1 2

L43 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN
Full Text:
AN 1986:473434 CAPLUS
DN 105:73434
TI The trfB region of broad host range plasmid RK2: the nucleotide sequence reveals incC and key regulatory gene trfB/korA/korD as overlapping genes
AU Thomas, Christopher M.; Smith, Christopher A.
CS Dep. Genet., Univ. Birmingham, Birmingham, B15 2TT, UK
SO Nucleic Acids Research (1986), 14(11), 4453-69
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The nucleotide sequence of the trfB region of broad host range plasmid RK2 is reported. This region encodes the following loci: trfB, identical to korA and korD, which encodes a key transcriptional repressor of certain RK2 operons; incC, which appears to be involved in plasmid maintenance, possibly through post-transcriptional regulation of trfA product levels; the start of korB, which encodes a 2nd transcriptional repressor of operons involved in stable inheritance of RK2. These loci are expressed as part of the trfB operon. In combination with deletion anal., transcriptional and translation fusions and maxicell anal. of polypeptides, the DNA sequence allows a no. of conclusions to be drawn. First, the korB ORF start codon overlaps the incC ORF stop codon, suggesting the possibility of translational coupling between these 2 genes. Second, the trfB ORF lies entirely within the 1st third of the incC ORF using a different phase. Third, the incC ORF appears to contain a 2nd transcriptional start whose function appears to be coupled to translation of the trfB ORF. Anal. of codon usage in the region of overlap between incC and trfB suggests that the incC gene may have evolved before the trfB gene. Detn. of the DNA sequence of a mutant in which the product of trfB is rendered defective for transcriptional repression

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reveals an amino acid alteration within a region of this polypeptide which exhibits homol. to the α helix-turn- α helix motif characteristic of many DNA binding proteins, and which is probably responsible for recognition of the trfB operator by this protein.

IT 88748-47-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 88748-47-4 CAPLUS

CN DNA (plasmid RK2 gene korA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagaaac ggcttaccga aagccagtgc caggaggcga tccagggct
51 ggaagtgggg cagcagacca tcgagatgc gcggggcgtc ttatcgatg
101 ggaagccaca ggcgacgttc gcaacgtcgc tggactgac cagggcgca
151 gtgtcgcaag cggtgcatcg cgtgtggcc gcgttcgagg acaaactt
201 gccccgagggg tacgcgcggg taacggcggt tctgcggaa catcaggcgt
251 acatcgctgg gaagtgggaa gcccaccca agaaaaaaca gaaaaaccaa
301 cgatga

L43 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:62573 CAPLUS

DN 100:62573

TI Map location and nucleotide sequence of korA, a key regulatory gene of promiscuous plasmid RK2

AU Bechhofer, David H.; Figurski, David H.
CS Dep. Microbiol., Coll. Phys. Surg., New York, NY, 10032, USA

SO Nucleic Acids Research (1983), 11(21), 7453-69

====

CODEN: NAFHAD; ISSN: 0305-1048

DT Journal

LA English

AB Earlier work showed that the korA gene of the broad-host-range plasmid RK2 is located within the 50.4-56.4 region. By addnl. subcloning of this region, korA was mapped to the segment between the HaeII site at 55.0 and the HincII site at 55.6. The direction of korA transcription (55.6 to 55.1) was detd. by 2 methods: (1) inactivation of korA expression signals and fusion of the structural gene to other promoters; and (2) hybridization anal. of korA-specific RNA synthesized in vivo. The nucleotide sequence of the korA region was detd. A potentially strong promoter overlaps the HincII site at 55.6, and there is a coding region which specifies the putative korA polypeptide. That this is the korA gene was supported by sequence anal. of Bal31-generated deletion mutants of korA. The sequence shows the korA product to be a small basic polypeptide of 101 amino acids.

IT 88748-47-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 88748-47-4 CAPLUS

CN DNA (plasmid RK2 gene korA) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atgaagaaac ggcttaccga aagccagtgc caggaggcga tccagggct
51 ggaagtgggg cagcagacca tcgagatgc gcggggcgtc ttatcgatg
101 ggaagccaca ggcgacgttc gcaacgtcgc tggactgac cagggcgca
151 gtgtcgcaag cggtgcatcg cgtgtggcc gcgttcgagg acaaactt
201 gccccgagggg tacgcgcggg taacggcggt tctgcggaa catcaggcgt

STN Columbus

251 acatcgctgg gaagtggaa gcggacgcca agaaaaaaca ggaaacccaaa
301 cgatga

| => file registry | | SINCE FILE | TOTAL |
|--|--|------------|---------|
| COST IN U.S. DOLLARS | | ENTRY | SESSION |
| FULL ESTIMATED COST | | 19.59 | 476.33 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | | SINCE FILE | TOTAL |
| CA SUBSCRIBER PRICE | | ENTRY | SESSION |
| | | -1.46 | -11.68 |

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*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added. *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s gtcagatcg/sqen
0 GTCAGATCG/SQEN
107453 SQL=9
L44 0 GTCAGATCG/SQEN
(GTCAGATCG/SQEN AND SQL=9)

=> s gtcagatcg/sqsn
L45 57217 GTCAGATCG/SQSN

=> s l45 and SQL<400
22713436 SQL<400
L46 5041 L45 AND SQL<400

STN Columbus

| | | | |
|--|------------------|---------------|--|
| => file caplus | | | |
| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION | |
| FULL ESTIMATED COST | 39.81 | 516.14 | |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION | |
| CA SUBSCRIBER PRICE | 0.00 | -11.68 | |

FILE 'CAPLUS' ENTERED AT 17:31:58 ON 29 APR 2005
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```
=> s 146
L47      1060 L46

=> s 147 and PY<1987
      11536051 PY<1987
L48      0 L47 AND PY<1987
```

| | | | |
|--|------------------|---------------|--|
| => file registry | | | |
| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION | |
| FULL ESTIMATED COST | 2.34 | 518.48 | |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION | |
| CA SUBSCRIBER PRICE | 0.00 | -11.68 | |

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 DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

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*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s atgaggct/sqen
      C ATGAGGGCT/SQEN
      107453 SQL=9
L49          0 ATGAGGGCT/SQEN
              (ATGAGGGCT/SQEN AND SQL=9)

=> s atgaggct/sqsn
L50      161522 ATGAGGGCT/SQSN

=> s l50 and SQL<400
      22713436 SQL<400
L51      12306 L50 AND SQL<400

=> file caplus
COST IN U.S. DOLLARS           SINCE FILE      TOTAL
                                ENTRY        SESSION
FULL: ESTIMATED COST          39.81         558.29

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE      TOTAL
                                              ENTRY        SESSION
CA SUBSCRIBER PRICE            0.00          -11.68
```

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

STN Columbus

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> S 151
L52 2438 L51

=> s 152 and PY<1987
11536051 PY<1987
L53 2 L52 AND PY<1987

=> d bib ab hitseq 1 2

1.53 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

ESSAYS

AN 1986:83873 CAPLUS

DN 104 : 83873

TI Synthesis and expression of the native RNase T1 gene and several mutant genes

AU Nishikawa, S.; Morioka, H.; Tokunaga, T.; Aoyama, Y.; Kikyotani, S.; Fujimoto, K.; Yanase, K.; Tanaka, T.; Uesugi, S.; et al.

Fujimoto, K.; Yanase, K.; Tanaka, T.; Uesugi, S.
Institute of Industrial Science, University of Tokyo, 2-6-1 Ohmachi, Chuo-ku, Tokyo 106, Japan

CS Fac. Pharm. Sci., Osaka Univ., Osaka, 565, Japan
SO Nucleic Acids Symposium Series (1985), 16(Symp. Nucleic Acids Chem., 1984), 227-230

13th), 287-90
CODEN: NACSD8; ISSN: 0261-3166

DT: Journal

LA English

AB RNase T1 gene and several mutant genes were constructed by joining of chem. synthesized deoxyoligonucleotides. These genes were inserted into an expression vector and expressed as fused protein in Escherichia coli. RNase T1 and its mutant enzymes were liberated by CNBr treatment and their activities were measured.

IT-07703-04-8

RL: FRP (Properties) (nucleotide sequence of)

RN 97708-04-8 CAPLUS

CN: DNA, d(G-A-T-C-T-T-C-A-T-G-G-C-T-T-G-C-G-A-C-T-A-C-A-C-C-T-G-C-G-G-C-A-G-C-A-A-C-T-G-C-T-A-C-G-G-A-A-C-T-G-C-T-A-C-T-C-T-A-G-C-T-C-T-G-A-C-G-T-T-C-T-A-C-C-G-C-T-C-A-G-G-C-T-G-C-T-G-G-C-T-A-C-C-A-G-C-T-G-C-A-C-G-A-G-G-A-C-G-G-C-G-A-A-A-C-C-G-T-T-G-G-C-T-C-T-A-A-C-T-C-T-T-A-C-C-C-G-C-A-C-A-A-T-A-C-A-A-C-A-C-T-A-T-G-A-G-G-G-C-T-T-C-G-A-C-T-T-A-G-C-G-T-T-C-T-T-C-T-C-G-T-A-C-T-A-C-G-G-A-A-T-G-G-C-C-G-A-T-C-C-T-G-T-C-T-A-G-C-G-G-C-G-A-C-G-T-T-T-A-C-T-C-C-G-G-A-A-T-G-G-C-C-G-A-T-C-C-T-G-T-C-T-A-G-C-G-G-C-G-A-C-G-T-T-T-A-C-T-C-C-G-G-T-C-C-A-G-G-T-A-G-T-A-T-T-C-A-A-C-G-A-A-A-C-C-A-G-C-T-C-G-C-T-G-G-C-G-T-T-A-T-C-A-C-C-C-A-C-A-C-C-G-G-C-G-C-T-T-C-G-G-C-A-A-C-A-A-C-T-T-G-T-A-G-A-A-T-G-C-A-C-C-C-T-A-A-G), complex with DNA d(T-C-G-A-C-T-A-T-T-A-G-G-T-G-C-A-T-T-C-T-A-C-A-A-G-T-T-G-C-G-C-C-A-G-C-G-G-T-G-T-G-G-T-G-A-T-A-A-C-G-C-C-A-G-C-G-A-C-C-T-G-G-T-T-G-T-T-C-G-T-T-G-A-A-T-A-C-T-A-C-A-C-G-G-T-C-A-G-C-A-C-C-G-C-T-A-C-C-C-T-G-G-A-C-C-G-G-A-G-T-A-C-G-G-C-C-A-T-T-C-G-T-A-G-T-A-C-G-G-A-G-A-A-G-A-A-C-G-C-T-A-A-A-G-G-A-T-C-G-G-C-C-A-T-T-C-G-T-A-G-T-A-C-G-G-A-G-A-A-G-A-A-A-C-G-C-T-A-A-A-G-T-C-G-A-A-G-C-C-C-T-C-A-T-A-G-T-T-G-T-T-G-T-A-T-T-T-G-T-G-C-G-G-G-T-A-A-G-A-G-T-T-A-G-C-C-C-T-C-A-T-A-G-T-T-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-A-G-C-C-A-G-C-C-T-G-A-G-C-C-T-G-G-T-T-C-G-C-C-G-G-T-C-T-C-G-T-G-C-A-G-C-T-G-G-T-A-A-G-A-G-T-C-G-C-A-A-G-C-C-A-T-G-A-A) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

```

SEQ      1 gatcttcatg gcttgcact acacctgcgg cagcaactgc tactctagc
        51 ctqacqtttc taccgctca gctgctggct accagctgca cgaggacggc

```

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101 gaaaccgtt gctctaactc ttacccgcac aaatacaaca actatgagg
151 ctgcacttt agcgtttctt ctcgtacta cgaatggccg atcctgtcta
201 gcggcgacgt ttactccggt ccaggttagcg gtgctgaccg tgttagtattc
251 aacgaaaaca accagctcgc tggcgttata acccacacccg gcgcttctgg
301 caacaacttt qtagaatgca cctaatacg

```
 1 tcgactatta ggtgcattct acaaaggtgt tgccagaagc gccggtgtgg  
 51 gtgataacgc cagcgagctg gttgtttcg ttgaatacta cacggtcagc  
101 accgctacct ggaccggagt aaacgtcgcc gctagacagg atcggccatt  
151 cgtagtaacgg agaagaaaacg ctaaaagtgcg agcctcata gttgttgat  
201 ttgtgcgggt aagagttaga gccaacggtt tcggccgtct cgtgcagctg  
251 gtagccagca gcctgagcgg tagaaacgtc agagctagag tagcagtgc  
301 tqcccqcaqgt qtaytcgcaa gccatgaa
```

1.53 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:432714 CAPLUS

DN 103:82714

TI Synthesis and expression of RNase T1 gene

AU Ikehara, M.; Ohtsuka, E.; Uesugi, S.; Kikyodani, T.; Aoyama, Y.; Tokunaga, T.; Fujimoto, K.

CS Fac. Pharm. Sci., Osaka Univ., Suita, 565, Japan

SO Nucleic Acids Symposium Series (1984), 15 (Symp. Nucleic Acids Chem.),

三三三三

197-200

CODEN: NACSD8; ISSN: 0261-3166

DT Journal

LA English

AB To obtain knowledge about the structure-function relation of RNase T1 [9026-12-4], a structural gene was synthesized for RNase T1 and several of its modified genes. Using amino acid codons frequently used in *Escherichia coli*, genes were designed that consist of 328×2 bases. Oligodeoxynucleotides with 9-20 base lengths were synthesized on a 1% polystyrene support and the resulting 42 oligomers were joined together using T4 DNA ligase. The product was analyzed and utilized to construct expression vectors, which produced effectively fused proteins.

IT 97708-04-8P

- RL: PREP (Preparation)

(prepn. cf. RNase T1 fusion protein expression from)

RN 97702-04-8 CAPLUS

STN Columbus

NTE doublestranded (2)

SEQ 1 gatttcatg gcttgcact acacctgcgg cagcaactgc tactctagct
51 ctgacgttc taccgcttag gctgctggct accagctgca cgaggacggc
101 gaaaccgttg gctctaactc ttacccgcac aaataacaaca actatgaggg
151 cttcgacttt agcgtttctt ctccgtacta cgaatgccg atcctgtcta
201 gcccgcacgt ttactccggc ccaggttagcg gtgctgaccg tgttagtattc
251 aacgaaaaca accagctgcg tggcgttatc acccacacccg gcgcctctgg
301 caacaacttt gtagaatgca cctaataag

1 tcgactattt ggtgcattct acaaagttgt tgccagaagc gccgggtgtgg
51 gtgataaacgc cagcgagctg gttgtttcg ttgaatacta cacggcagc
101 accgctacct ggaccggagt aaacgtgcgc gctagacagg atccggcatt
151 cgtagtaagg agaagaaaacg ctaaagtcg agccctata gtttgttat
201 ttgtgcgggt aagagttaga gccaacgggt tcgcccgtcct cgtgcagctg
251 gtagccagca gcctgagcgg tagaaacggtc agagctagag tagcagttgc
301 tgccgcagggt gtagtcgcaa gccatgaa

| => file registry | SINCE FILE | TOTAL |
|--|------------|---------|
| COST IN U.S. DOLLARS* | ENTRY | SESSION |
| FULL ESTIMATED COST | 18.69 | 576.98 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE | TOTAL |
| CA SUBSCRIBER PRICE | ENTRY | SESSION |
| | -1.46 | -13.14 |

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* The CA roles and document type information have been removed from *
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* effective March 20, 2005. A new display format, IDERL, is now *
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*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more

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information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s atgaggcacg/sqsn
L54 91801 ATGAGCACG/SQSN

=> s l54 and SQL<400
22713436 SQL<400
L55 6980 L54 AND SQL<400

| | SINCE FILE ENTRY | TOTAL SESSION |
|--|------------------|---------------|
| COST IN U.S. DOLLARS | 32.53 | 609.51 |
| FULL ESTIMATED COST | | |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -13.14 |

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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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=> s l55
L56 1660 L55

=> s l55 and PY<1987
1660 L55
11536051 PY<1987
L57 2. L55 AND PY<1987

=> d bib ab hitseq 1 2

L57 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:210702 CAPLUS
DN 98:210702
TI Nucleotide sequence of bacteriophage λ DNA
AU Sanger, F.; Coulson, A. R.; Hong, G. F.; Hill, D. F.; Petersen, G. B.
CS Lab. Mol. Biol., Med. Res. Cent., Cambridge, CB2 2QH, UK
SO Journal of Molecular Biology (1982), 162(4), 729-73

STN Columbus

CODEN: JMOBAK; ISSN: 0022-2836

DT Journal

LA English

AB The nucleotide sequence of the DNA of phage λ was detd. by using the dideoxy chain termination method in conjunction with random cloning in phage M13 vectors. Various methods were studied for sequencing specific regions to complete the sequence, but all were much slower than the random approach. The DNA in its circular form contains 48,502 base pairs. Open reading frames were identified and, where possible, ascribed to genes by comparing with the previously detd. genetic map. The reading frames for 46 genes were clearly identified, though in ~20, the position of the protein initiation site could not be rigorously established. Probable positions for the kil, cIII, and lom genes are suggested but remain uncertain. There are ~20 other unidentified reading frames that may code for proteins. The genome is fairly compact with comparatively little noncoding DNA. In many cases, the translation terminators and initiators overlap, particularly in the sequence A-T-G-A where the TGA terminates 1 gene and the ATG initiates the next. Such structures seem to be characterized by a purine-rich sequence, rather than by a specific Shine and Dalgarno sequence, before the initiator. In the whole of the left arm, the codon CTA, which is normally read by a minor leucine tRNA, is absent. The distribution of other rare codons in the genes of the left arm suggests that they may have a controlling function of the relative amounts of the proteins produced.

IT 84616-07-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 84616-07-9 CAPLUS

CN DNA (coliphage λ gene ren) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ: 1 atgacgggc~~a~~ aagaggcaat tattcattac ctggggacgc ~~t~~ataatagctt
51 ctgtgcgc~~c~~ gacgttgc~~c~~ cgctaacagg cgcaacagta accagcataa
101 atcaggccgc ggctaaaatg gcacgggc~~a~~ gtcttcgtt tattcgaaggt
151 ~~z~~agg~~t~~ctggc gaacggtgta ttaccgg~~t~~tt gctaccagg~~a~~ aagaacggga
201 aggaaagatg agcacgaacc tgat~~tttt~~aa ggagtgtcg~~c~~ cagagtgc~~c~~
251 cgatgaaacg ggtattggc~~g~~ gtatatggag taaaagatg a

L57 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:66402 CAPLUS

DN 98:66402

TI A chain of interlinked genes in the ninR region of bacteriophage lambda

AU Kroeger, Manfred; Hobom, Gerd

CS Inst. Biol. III, Univ. Freiburg, Freiburg/Br., D-7900, Fed. Rep. Ger.

SO Gene (1982), 20(1), 25-36

====

CODEN: GENED6; ISSN: 0378-1119

DT Journal

LA English

AB The 3612-base-pair (bp) DNA sequence of the phage λ -P-Q (ninR) region contains a series of 9 open reading frames in a distinctly overlapping pattern: ATGA sequence modules occur at the boundaries of consecutive genes and are able to serve both as terminator (TGA) and (re)initiator (ATG) codons for most of the adjacent frames. Together with genes O, P, and Q, the newly detected ren and ninA through ninH constitute a series of 12 closely linked genes in the PR operon. The available evidence for several of the nin proteins, and plasmid expression data,

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suggest that at least the larger nin genes, and probably all of the newly detected open reading frames, code for proteins. The nin5 deletion of 2803 bp is a frame-to-frame fusion of ren and ninH, and covers the tR2 termination signal located near its left boundary, immediately behind the ren gene. The possible significance of the obsd. chain of closely interlinked genes for the regulation of Q expression is discussed.

IT 84616-07-9

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN: 84616-07-9 CAPLUS

CN: DNA (coliphage λ gene ren) (9CI) (CA INDEX NAME)

NTE: doublestranded

SEQ: 1 atgacggca aagaggcaat tattcattac ctggggacgc ataatacgct
51 ctgtgcggcg gacgttgcgg cgctaaccagg cgcaacagta accagcataa
101 atcaggccgc ggctaaaatg gcacgggcag gtcttcgggt tatcgaagg
151 aaggcttgcgaaacggta ttaccgggtt gctaccagg aagaacggga
201 aggaaagatg agcaccaacc tgattttaa ggagtgtcgc cagagtggcg
251 cgatgaaacg ggtattggcg gtatatggag ttaaaatggat a

=> file registry

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|----------------------|------------------|---------------|
| FULL ESTIMATED COST | 18.69 | 628.20 |

| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
|--|------------------|---------------|
| CA SUBSCRIBER PRICE | -1.46 | -14.60 |

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* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

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Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s ggcgtgaac/sqsn
L58 132811 GGC GTGAAC/SQSN

=> s 158 and SQL<400
22713436 SQL<400
L59 11658 L58 AND SQL<400

| | | |
|--|------------------|---------------|
| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
| FULL ESTIMATED COST | 32.53 | 660.73 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -14.60 |

FILE 'CPLUS' ENTERED AT 17:39:48 ON 29 APR 2005
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FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 159
L60 1532 L59

=> s 160 and PY<1987
11536051 PY<1987
L61 0 L60 AND PY<1987

| | | |
|--|------------------|---------------|
| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
| FULL ESTIMATED COST | 2.34 | 663.07 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -14.60 |

STN Columbus

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STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more
information, enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> s atgatgatg/sqsn
L62 663450 ATGATGATG/SQSN

=> s l62 and SQL<400
22713436 SQL<400
L63 61649 L62 AND SQL<400

| | SINCE FILE ENTRY | TOTAL SESSION |
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| COST IN U.S. DOLLARS | 32.53 | 695.60 |
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| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -14.60 |

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FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> S 163
L64 5122 L63

=> S 164 and PY<1987
11536051 PY<1987
L65 11 L64 AND PY<1987

=> d bib ab hitseq 1-11

L65 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1989:19409 CAPLUS
DN 110:19409
TI Bacterial expression vectors containing lipoprotein gene 5' sequences
IN Mayne, Nancy G.; Burnett, J. Paul; Belegaje, Ramamoorthy; Hsiung, Hansen
M.

PA Eli Lilly and Co., USA
SO U.S., 21 pp. Cont.-in-part of U.S. Ser. No. 381,992, abandoned.
CCDEN: USXXAM

DT Patent
LA English

FAN.CNT 2

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------------|------|----------|-----------------|--------------|
| PI US 4745069 | A | 19880517 | US 1984-586581 | 19840306 |
| HU 31783 | O | 19840528 | HU 1983-1810 | 19830523 <-- |
| HU 197349 | B | 19890328 | | |
| PRAI US 1982-361992 | A2 | 19820525 | | |

AB A plasmid for efficient expression of exogenous genes comprises the 5' untranslated region and promoter of the lipoprotein (lpp) gene operably linked to a translation start codon, a sequence encoding an enterokinase cleavage site, and the gene for the exogenous protein, as well as a replicon and ≥1 genes for selectable markers. Plasmid pCC101, contg. the Escherichia coli lpp gene 5' untranslated sequence and promoter and a gene encoding an enterokinase cleavage peptide fused to bovine growth hormone, was constructed. Fusion protein 240 mg was obtained from 22 g E. coli transformed with the plasmid. The biol. activity of the growth hormone released by enterokinase cleavage was comparable to that of a bovine growth hormone obtained from the National Pituitary Agency (as measured by proximal tibia epiphyseal cartilage growth in hypophysectomized female rats).

IT 119145-54-3

RL: PRP (Properties)
(enterokinase cleavage site-encoding double-stranded DNA, lipoprotein gene promoter-contg. microbial expression plasmids in relation to)

RN 118145-54-3 CAPLUS

CN Guanosine, 2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')

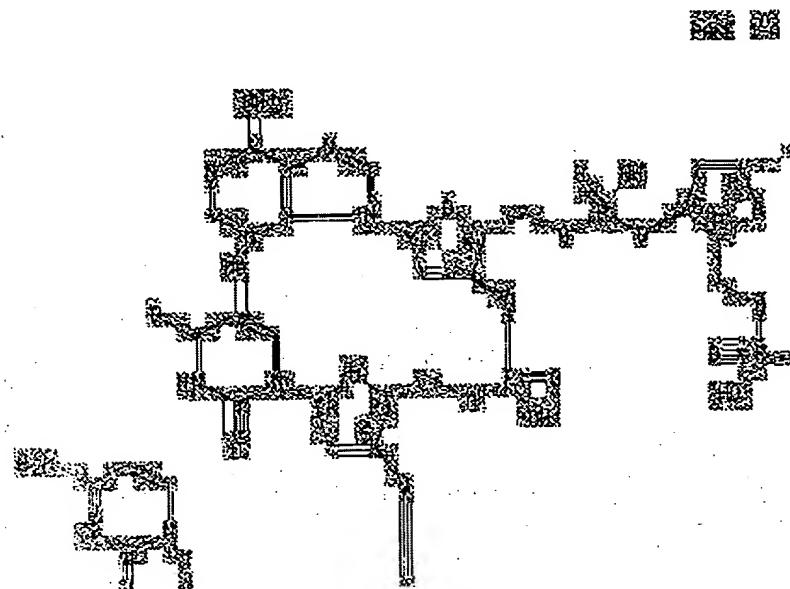
STN Columbus

2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxyguanylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-adenylyl-(3'→5')-2'-deoxy-, complex with 2'-deoxycytidyl-(3'→5')-thymidylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidyl-(3'→5')-2'-deoxyadenylyl-(3'→5')-thymidylyl-(3'→5')-2'-deoxycytidine (1:1) (9CI) (CA INDEX NAME)

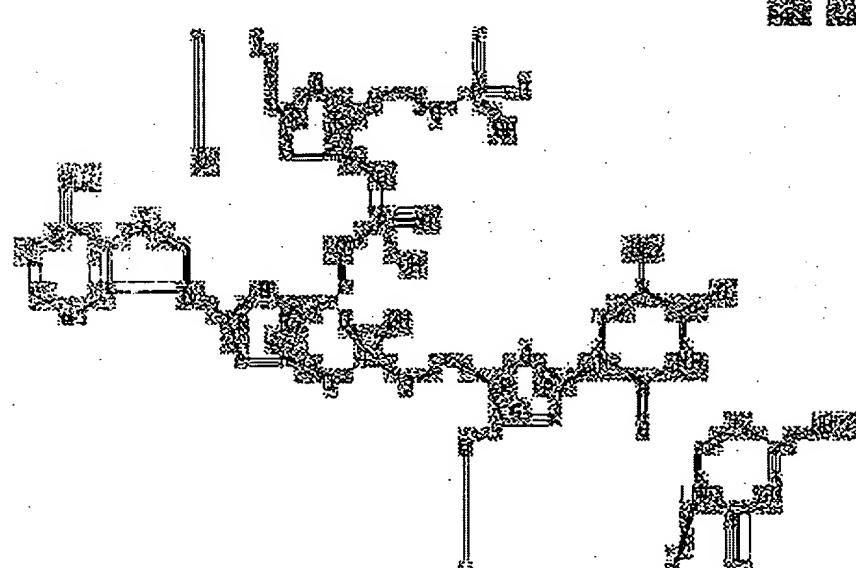
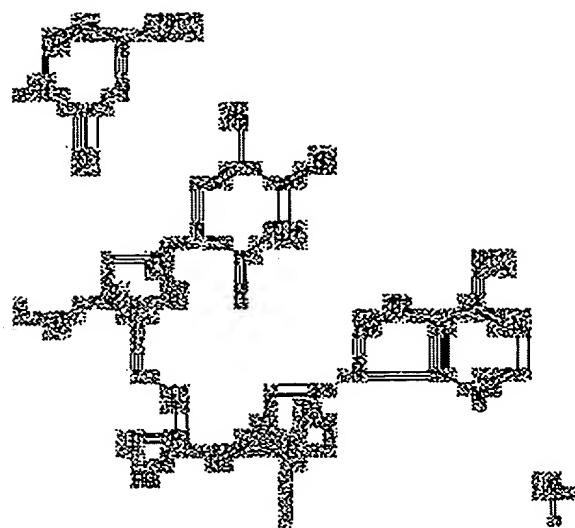
CM 1

CRN 118145-53-2
CMF C116 H150 N37 O72 P11

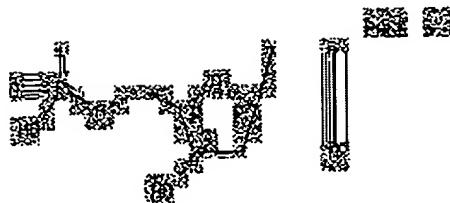
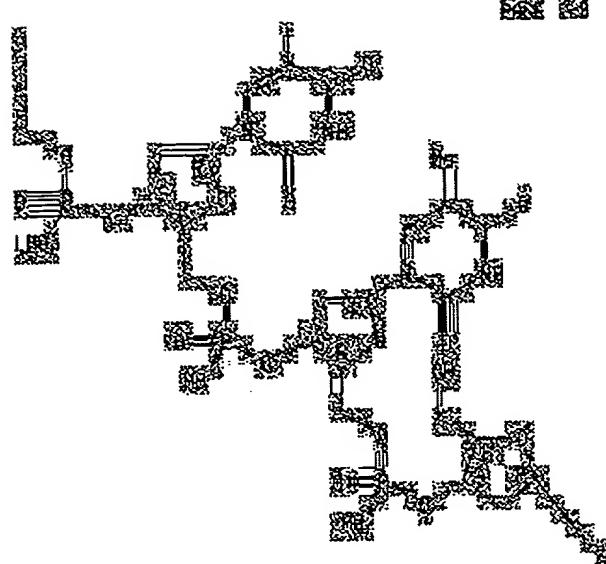
Absolute stereochemistry.



STN Columbus



STN Columbus



STN Columbus

CM 2

CRN 89233-95-4
CMF C150 H185 N63 O86 P14
CCI MAN

STRUCTURE DIAGRAM IS NOT AVAILABLE
IT 89382-91-2 89382-93-4

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, lipoprotein gene promoter-contg. microbial
expression plasmids contg.)

RN 89382-91-2 CAPLUS
CN DNA, d(C=G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-
A-T-C-C-A-A-T-G-G-A-A-C-A-T-T-A-T-A-A-T-A-C-C-C-T), complex with DNA
d(C-T-A-G-A-G-G-G-T-A-T-A-A-T-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-
T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA
INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctagagggtta ttaataatgt tcccatttggaa tgatgtatgt aagttcccaag
51 ccatgtcctt gtc

1 cggacaagga catggctggg aacttatcat catcatccaa tggaaacatt
51 attaataacc t

RN 89382-93-4 CAPLUS
CN DNA, d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-
G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-A-T-C-C-A-G-G-C-T-T-T-
T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA
d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-C-A-A-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-A-
A-T-C-G-T-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-C-A-T-C-C-A-A-T-G-G-A-A-C-A-
T-T-A-T-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctagagggtta ttaataatgt tcccatttggaa tgatgtatgt aagttcccaaa
51 ccattccctt atccaggctt tttgacaacg ctatgtcccg

1 cggagcatag cgttgtcaaa aagcctggat aaggaaatgg ttggaaactt
51 atcatcatca tccaatggga acattattaa tacccct

STN Columbus

L65 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1987:1101 CAPLUS

DN 106:1101

TI Origin of transfer of IncF plasmids and nucleotide sequences of the type II oriT, traM, and traY alleles from ColB4-K98 and the type IV traY allele from R100-1

AU Finlay, B. Brett; Frost, Laura S.; Paranchych, William

CS Dep. Biochem., Univ. Alberta, Edmonton, AB, T6G 2H7, Can.

SO Journal of Bacteriology (1986), 168(1), 132-9

====

CODEN: JOBAAY; ISSN: 0021-9193

DT Journal

LA English

AB The complete nucleotide sequences of the ColB4-K98 (ColB4) plasmid transfer genes oriT, traM, and traY as well as the traY gene of plasmid R100-1 are presented and compared with the corresponding regions from the conjugative plasmids F, R1, and R100. The sequence encoding the oriT nick sites and surrounding inverted repeats identified in F was conserved in ColB4. The adenine-thymine-rich sequence following these nick sites was conserved in R1 and ColB4 but differed in F and R100, indicating that this region may serve as the recognition site for the traY protein. A series of direct repeats unique to the ColB4 plasmid was found in the region of dyad symmetry following this AT-rich region. This area also encodes 21-base-pair direct repeats which are homologous to those in F and R100. The traM gene product may bind in this region. Overlapping and following these repeats is the promoter(s) for the traM protein. The traM protein from ColB4 is similar to the equiv. products from F, R1, and R100. The traY protein from ColB4 is highly homologous to the R1 traY gene product, while the predicted R100-1 traY product differs at several positions. These differences presumably define the different alleles of traM and traY previously identified for IncF plasmids by genetic criteria. The translational start codons of the ColB4 and R100-1 traY genes are GUG and UUG, resp., 2 examples of rare initiator codon usage.

IT 105647-44-7

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 105647-44-7 CAPLUS

CN DNA (plasmid pED203 gene traM) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1-atggccagag taaaatctgta tatcagtaat gaggttcatg aaaaaattaa
51 catgattgtt gaaaaagcgctc gtcaggaggg agcaagagat aaagatataa
101 gcctttcagg aactgcttca atgcttcttg aattggggct tcgcgtatata
151 gatgcacaga tggagcgtaa agagtctgcg tttaaccaga cagagttaa
201 taaaacttctt cttgaatgtg ttgtaaaaac acagtcAACG gtggcuaaga
251 ttttaggtat tgagtctctc agtcctcatg tctccggaaa cccgaagttt
301 gaatatgccca gtatgggtga cgatatcaga gagaaagtgt ctgttgagat
351 ggaccggttt tttccaaaaaa atgatgtga ataaatga

L65 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1986:181124 CAPLUS

DN 104:181124

TI Heat shock promoter and gene

IN Key, Joe L.; Gurley, William B.; Nagao, Ronald T.; Schoeffl, Friedrich; Czarnecka, Eva

PA Agrigenetics Research Associates Ltd., USA

STN Columbus

SO Eur. Pat. Appl., 52 pp.
CODEN: EPXXDW

DT Patent
LA English

FAN.CNT 1

PATENT

三三三

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|---|------|----------|-----------------|-------------|
| PI | EP 159884 | A2 | 19851030 | EP 1985-302593 | 19850412 <- |
| | EP 159884 | A3 | 19871125 | | |
| | EP 159884 | B1 | 19930210 | | |
| | R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE | | | | |
| | US 5447858 | A | 19950905 | US 1984-599993 | 19840413 |
| | CA 1338010 | A1 | 19960130 | CA 1985-478916 | 19850411 |
| | JP 60248176 | A2 | 19851207 | JP 1985-79127 | 19850412 <- |
| | AT 85650 | E | 19930215 | AT 1985-302593 | 19850412 |
| | JP 07075567 | A2 | 19950320 | JP 1994-73623 | 19940412 |
| PRAI | US 1984-599993 | A | 19840413 | | |
| | EP 1985-302593 | A | 19850412 | | |

AB EP 1985-302395 A 1989-11
Four heat shock genes of soybean were cloned and sequenced. The heat shock promoter fragments of these 4 heat shock genes were subcloned and genetically engineered into a T-DNA shuttle vector. These recombinant vectors were then transferred with the aid of a helper plasmid into Agrobacterium tumefaciens where the recombinant DNA fragment was integrated into the Ti-plasmid. The T-DNA portion of the Ti-plasmid could then be transferred to a plant genome. Thus, the gene for β -galactosidase under the control of a soybean heat shock gene promoter was inserted into a T-DNA shuttle vector, p233G, and the recombinant plasmid was used to transform Escherichia coli. In a triple mating involving a helper plasmid in an E. coli strain, the recombinant T-DNA shuttle vector was transferred in another E. coli strain, and a Ti-plasmid in A. tumefaciens. The recombinant T-DNA shuttle vector was transferred into A. tumefaciens and the recombinant gene was incorporated into the Ti-plasmid. When plant cell cultures were infected with the A. tumefaciens carrying the recombinant Ti-plasmid the T-DNA was transferred to the plant genome. Transformed plant cells were detectable by the transient appearance of a blue color when the cells were subjected to heat shock in 5-bromo-4-chloro-3-indcyl- β -D-galactoside.

TT 102036-84-0 102036-85-1

RL: PRP (Properties)

(heat shock protein gene promoter encoding, of soybean)

RN 102036-84-0 CAPLUS

RN 102338-01-0 C101
 CN DNA, d(A-G-A-C-C-A-A-T-C-C-T-A-A-C-C-A-A-T-G-T-C-T-G-G-T-T-A-A-G-A-T-G-G-T-
 C-C-A-A-T-C-C-C-G-A-A-A-C-T-T-C-T-A-G-T-T-G-C-G-G-T-T-C-G-A-A-G-A-A-G-C-C-
 A-G-A-A-T-G-T-T-C-T-G-A-A-A-G-T-T-C-A-G-A-A-A-A-T-T-C-T-A-G-T-T-T-G-
 A-G-A-T-T-T-C-A-G-A-A-G-T-A-C-G-G-C-A-T-G-A-T-G-A-T-G-C-A-T-A-A-C-A-A-G-
 G-A-C-T-T-C-T-C-G-A-A-A-G-T-A-C-T-A-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-
 T-T-T-T-A-A-A-T-A-C-C-C-C-A-T-G-T-G-T-C-C-T-T-G-A-A-G-A-C-A-C-A-T-C-A-C-
 A-G-A-A-A-G-A-A-G-T-G-A-A-G-G-G-C-A-T-C-G-T-T-A-G-C-A-G-T-T-T-G-T-A-G-A-T-
 T-C-A-A-C-C-T-C-A-A-T-T-T-G-C-A-G-A-G-T-T-A-C-G-T-T-C-T-A-A-T-A-T-A-T-T-
 A-C-A-C-A-A-G-A-C-T-G-A-C-C-C) (9CI) (CA INDEX NAME)

NTE singlestranded

| SEQ | 1 | agaccaatcc | taaccatatgt | ctggttaaga | tggccaatc | ccgaaacttc |
|-----|-----|------------|-------------|------------|-------------|-------------|
| | 51 | tagttgcgt | tcgaagaaggc | cagaatgttt | ctgaaaagttt | cagaaaattc |
| | 101 | tagtttgag | attttcgaaa | gtacggcatg | atgatgcata | acaaggactt |
| | 151 | tctcgaaagt | actatattgc | tcctctacat | cattttaaat | accccatgtt |
| | 201 | tcctttgaag | acacatcaca | gaaagaagtg | aaggcatcgt | tagcagtttt |
| | 251 | gtagattcaa | cctcaatttg | cagagttacg | ttctaataata | tttacacaaga |
| | 301 | actgacccc | | | | |

STN Columbus

RN 102036-85-1 CAPLUS
CN DNA, d(A-G-A-C-C-A-A-T-C-C-T-A-A-C-C-A-A-T-G-T-C-T-G-G-T-T-A-A-A-G-A-T-G-G-T-C-C-A-A-T-C-C-C-G-A-A-A-C-T-T-C-T-A-G-T-T-G-C-G-G-T-T-C-G-A-A-G-A-A-G-C-C-A-G-A-A-T-G-T-T-C-T-G-A-A-A-G-T-T-C-A-G-A-A-A-A-T-T-C-T-A-G-T-T-T-G-A-G-A-T-T-C-A-G-A-A-G-T-A-C-G-G-C-A-T-G-A-T-G-C-A-T-A-A-C-A-A-G-G-A-C-T-T-C-T-C-G-A-A-A-G-T-A-C-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-T-T-T-A-A-A-T-A-C-C-C-C-A-T-G-T-G-T-C-C-T-T-G-A-A-G-A-C-A-C-A-T-C-A-C-T-T-T-A-A-G-A-A-G-T-G-A-A-G-G-C-A-T-C-G-T-T-A-G-C-A-G-T-T-T-G-T-A-G-A-T-T-C-A-C-C-T-C-A-G-A-A-G-T-A-C-T-A-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-T-T-T-A-A-A-T-A-C-C-C-C-A-T-G-T-G-T-C-C-T-T-G-A-A-G-A-C-A-C-A-T-C-A-C-A-G-A-A-A-G-A-A-G-T-G-A-A-G-G-C-A-T-C-G-T-T-A-G-C-A-G-T-T-T-G-T-A-G-A-T-T-C-A-C-C-T-C-A-A-T-T-T-G-C-A-G-A-G-T-T-A-C-G-T-T-C-T-A-A-T-A-T-A-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-C-T-T-T-A-A-C-C-C-C-A-T-G-T-G-T-C-C-T-T-G-A-A-G-A-C-A-C-A-T-C-A-C-A-G-A-A-A-G-A-A-G-T-G-A-A-G-G-C-A-T-C-G-T-T-A-G-C-A-G-T-T-T-G-T-A-G-A-T-T-C-A-C-C-T-C-A-A-T-T-T-G-C-A-G-A-G-T-T-A-C-G-T-T-C-T-A-A-A-T-A-T-A-T-A-T-T-G-C-T-C-C-T-C-T-A-C-A-T-C-A-C-T-T-T-A-A-C-C-A-A-G-A-C-T-G-A-T-A-A-G-A-G-A-A-G-A-A-A-A-T-G-T-C-T-C-T-G-A-T-T-C-C-A-G-T-T-T-G-T-A-C-C-C-C-G-T-T-T-C-T-C-G-G-T-G-G-C-C-G-A-A-G-G-G-A-G-C-A-G-T-G-T-T-T-C-G-A-C-C-C-G-T-T-T-C-T-C-C-G-A-A-T-G-T-G-G) (9CI) (CA INDEX NAME)

NTE singlestranded

| | |
|-----|--|
| SEQ | 1 agaccaatcc taaccaatgt ctggtaaaga tggccaatc ccgaaacttc
51 tagttgcgt tcgaagaagc cagaatgtt ctgaaaagttt cagaaaattc
101 tagtttgag atttcagaa gtacggcatg atgatgcata acaaggactt
151 tctcgaaagt actatattgc tcctctacat cattttaat accccatgtg
201 tccttgaag acacatcaca gaaagaagtg aaggcatcgt tagcagtttt
251 gtagattcaa cctcaatttg cagagttacg ttctaataata tttacacaag
301 actgataaga gaaaatgtct ctgattccaa gtttcttcgg tggccgaagg
351 agcagtgttt tcgaccctt ctccctcgat gtgtgg |
|-----|--|

L65 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1986-181123 CAPLUS

DN 104:101-123

T1 Vectors for expressing bovine growth hormone derivatives

IN Ksiumg, Hansen Maxwell; Schoner, Ronald George; Schoner, Brigitte
Elisabeth

PA : Eli Lilly and Co., USA

SO Eur. Pat. Appl., 105 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

PATE

| PI | EP 159123 | A2 | 19851023 | EP 1985-301468 | 19850304 <-- |
|------|---|----|----------|-----------------|--------------|
| | EP 159123 | A3 | 19870722 | | |
| | EP 159123 | B1 | 19920115 | | |
| | R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE | | | | |
| | ZA 8501625 | A | 19861029 | ZA 1985-1625 | 19850304 <-- |
| | AT 71659 | E | 19920215 | AT 1985-301468 | 19850304 |
| | SU 1838412 | A3 | 19930830 | SU 1985-3867006 | 19850304 |
| | DK 8501000 | A | 19850907 | DK 1985-1000 | 19850305 <-- |
| | AU 8539503 | A1 | 19850912 | AU 1985-39503 | 19850305 <-- |
| | AU 590716 | B2 | 19891116 | | |
| | HU 38673 | A2 | 19860630 | HU 1985-835 | 19850305 <-- |
| | HU 202281 | B | 19910228 | | |
| | ES 540935 | A1 | 19870416 | ES 1985-540935 | 19850305 |
| | JP 61001391 | A2 | 19860107 | JP 1985-45685 | 19850306 <-- |
| | CN 85101561 | A | 19860910 | CN 1985-101561 | 19850401 <-- |
| | ES 550873 | A1 | 19871116 | ES 1986-550873 | 19860114 |
| | CA 1291718 | A2 | 19911105 | CA 1989-587903 | 19890110 |
| PRAI | US 1984-586582 | A | 19840306 | | |
| | US 1984-634920 | A | 19840726 | | |

STN Columbus

US 1985-697090 A 19850131
 EP 1985-301468 A 19850304
 CA 1985-475731 A3 19850305

AB Recombinant expression vectors are prep'd. that comprise a runaway replicon and a transcriptional and translational activating sequence which is in the reading frame of a gene that codes for a bioactive bovine growth hormone (bGH) deriv. By cloning the bGH deriv. gene into vectors contg. a runaway replicon it is possible to induce loss of copy no. control. This results in a greatly increased rate of protein synthesis and the concomitant formation of a species of intracellular proteinaceous granule. These granules are highly homogeneous in their protein compn. and are thus distinguishable over known high-mol.-wt. aggregates and inclusions that sometimes occur in recombinant DNA-contg. host cells. Recombinant vectors contg. synthetic genes encoding thymosin α_1 , and human proinsulin and a runaway replicon were also prep'd.

IT 89382-91-2P 89382-93-4P

RL: PREP (Preparation)
 (prep'n. of, as linker sequence for construction of bovine growth hormone plasmid vectors)

RN 89382-91-2 CAPLUS

CN DNA; d(C-G-G-A-C-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T), complex with DNA d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 cttagagggtta ttataatgt tcccatggta tgatgtatgt aagttccccag
 51 ccattgcctt gtc
 1 cggacaagga catggctggg aacttatcat catcatccaa tggAACATT
 51 tttaataccs t

RN 89382-93-4 CAPLUS

CN DNA; d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-T-A-T-C-C-A-G-G-C-T-T-T-T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-A-G-C-C-T-G-G-A-T-A-G-G-A-T-G-C-T-T-G-G-A-A-C-T-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-T-T-A-T-A-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 cttagagggtta ttataatgt tcccatggta tgatgtatgt aagttccccaa
 51 ccattgcctt atccaggctt tttgacaacg ctatgtcccg
 1 cggagcatag cgttgtcaaa aagcctggat aaggaaatgg ttggaaactt
 51 atccatcatca tccaatggta acattattaa taccct

I.65 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text:

AN 1996:63384 CAPLUS

DN 104:63384

TI Recombinant DNA expression vectors and method for gene expression

IN Schoner, Ronald George; Schoner, Brigitte Elisabeth

PA Eli Lilly and Co., USA

STN Columbus

SO Eur. Pat. Appl., 118 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------|---|------|----------|-----------------|--------------|
| PI | EP 154539 | A2 | 19850911 | EP 1985-301469 | 19850304 <-- |
| | EP 154539 | A3 | 19861230 | | |
| | R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE | | | | |
| | ZA 8501626 | A | 19861029 | ZA 1985-1626 | 19850304 <-- |
| | SU 1491346 | A3 | 19890630 | SU 1985-3862498 | 19850304 |
| | DK 9500999 | A | 19850907 | DK 1985-999 | 19850305 <-- |
| | AU 8539502 | A1 | 19850912 | AU 1985-39502 | 19850305 <-- |
| | AU 589355 | B2 | 19891012 | | |
| | HU 40162 | A2 | 19861128 | HU 1985-836 | 19850305 <-- |
| | HU 202587 | B | 19910328 | | |
| | ES 540936 | A1 | 19880501 | ES 1985-540936 | 19850305 |
| | CA 1283374 | A1 | 19910423 | CA 1985-475732 | 19850305 |
| | JP 61001387 | A2 | 19860107 | JP 1985-45684 | 19850306 <-- |
| | CN 85101555 | A | 19870124 | CN 1985-101555 | 19850401 |
| | ES 550013 | A1 | 19870101 | ES 1985-550013 | 19851216 |
| | ES 550012 | A1 | 19870601 | ES 1985-550012 | 19851216 |
| PRAI | US 1984-586592 | A | 19840306 | | |

AB Recombinant DNA expression vectors which allow far more efficient gene expression are constructed. Thus, a XbaI-HgiAI DNA linker sequence was ligated to the ~10.2 kb BamHI-XbaI and ~0.6 kb BamHI-HgiAI fragments of plasmid pCZ101 to yield pCZ114. Plasmid pCZ114 contains, in sequence, the Escherichia coli lipoprotein gene transcriptional and translational activating sequences, a DNA sequence encoding the peptide Met-Phe-Pro-Leu-Glu-Asp-Asp, a stop codon, and a translational start signal which is immediately adjacent to and downstream from the stop signal and which is in the reading frame of a nucleotide sequence coding for methionyl-bovine growth hormone. Vectors are also constructed in which synthetic genes for thymosin α 1 [62304-98-7] and human proinsulin [9035-68-1] were cloned, pTH α 1 and pH17 Δ 4 Δ 1, resp.

IT 89382-91-2P 89382-93-4P

RL: PREP (Preparation)
(prepn. of)

RN 89382-91-2 CAPLUS

CN DNA, d(C-G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-A-T-G-G-A-C-A-T-G-G-G-A-A-C-A-T-T-A-T-A-T-A-C-C-C-T), complex with DNA d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-G-T-C) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctagaggta ttaataatgt tcccattgga tgatgtatgt aagttcccg
51 ccatgtcctt gtc

1 cggacaagga catggctggg aacttatcat catcatccaa tggaaacatt
51 attaataacc t

RN 89382-93-4 CAPLUS

CN DNA, d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-C-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-A-T-C-C-C-A-G-G-C-T-T-T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-A-

STN Columbus

A-T-G-G-T-T-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-
T-T-A-T-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ . 1 ctagaggta ttaataatgt tcccattgga tgatgatgat aagttcccaa
. 51 ccattccctt atccaggctt ttgacaacg ctatgctccg

1 cggyacatag cgttgtcaaa aagcctggat aaggaaatgg ttgggaactt
51 atcatcatca tccaatggga acattattaa tacccct

L65 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1985:180056 CAPLUS

DN 102:180056

TI A single rearrangement event generates most of the chicken immunoglobulin light chain diversity

AU Reynaud, Claude Agnes; Anquez, Viviane; Dahan, Auriel; Weill, Jean Claude
CS Groupe Immunodifferentiation Mol., Inst. Jacques Monod, Paris, 75251, Fr.

SO Cell (Cambridge, MA; United States) (1985), 40(2), 283-91

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CODEN: CELLB5; ISSN: 0092-8674

DT Journal

LA English

AE The chicken Ig λ locus contains a single Cλ gene with a unique Jλ element, 1.9 kilobases (kb) upstream. The same Vλ gene (Vλ1) is rearranged in most cells of the Bursa of Fabricius. This Vλ1 gene is located, in germ-line configuration, 1.7 kb upstream from Jλ and in the same transcriptional orientation. Eight to 12 variable genes of the same set are found adjacent to the Vλ1 gene, indicating that V-gene amplification did occur. Three of these genes were sequenced and proved to be pseudogenes, one of them having an inverted polarity. Data suggesting extensive somatic diversification of the Vλ1 sequence are reported, including the possible use of nonfunctional V elements in a somatic gene-conversion-like process.

IT 96119-15-2

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 96119-15-2 CAPLUS

CN DNA (chicken immunoglobulin Vλ1 pseudogene ψV1) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ . 1 gagggccctgt gccccgcagcc acatgtggaa tatcaagaca cacacatcta
. 51 tgacaatcac aacctgatca tcaaccacta tggctggatc cagcagaggg
101 cacctggcag tgccccctgtc actctgatct actatgatga tgagagaccc
151 tcgaacatcc cttcacgatt ctccgggtcc aaatccggct ccacacacac
201 tttaaccatc actggggatcc aagccgacga cgaggctgtc tattactgt
251 ggaatgaaga cagcagcggt actggat

L65 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:605037 CAPLUS

DN 101:205037

STN Columbus

TI Nucleotide sequence encoding the flavoprotein and hydrophobic subunits of the succinate dehydrogenase of Escherichia coli
AU Wood, David; Darlison, Mark G.; Wilde, Robin J.; Guest, John R.
CS Dep. Microbiol., Sheffield Univ., Sheffield, S10 2TN, UK
SO Biochemical Journal (1984), 222(2), 519-34

====

CODEN: BIJOAK; ISSN: 0306-3275

DT Journal

LA English

AB The nucleotide sequence of a 3614-base-pair (bp) segment of DNA contg. the *sdhA* gene, encoding the flavoprotein subunit of succinate dehydrogenase [9002-02-2] of *E. coli*, and the 2 genes *sdhC* and *sdhD*, encoding small hydrophobic subunits, was detd. Together with the Fe-S protein gene (*sdhP*), these genes form an operon (*sdhCDAB*) situated between the citrate synthase gene (*gltA*) and the 2-oxoglutarate dehydrogenase complex genes (*sucAB*): *gltA-sdhCDAB-sucAB*. Transcription of the *gltA* and *sdhCDAB* gene appears to diverge from a single intergenic region that contains 2 pairs of potential promoter sequences and 2 putative cAMP receptor protein-binding sites. The *sdhA* structural gene comprises 1761 bp (587 codons, excluding the initiation codon AUG), and it encodes a polypeptide of 64,263 mol. wt. that is strikingly homologous with the flavoprotein subunit of fumarate reductase (the *frdA* gene product). The FAD-binding region, including the histidine residue at the FAD-attachment site, was identified by its homol. with other flavoproteins and with the flavopeptide of the bovine heart mitochondrial succinate dehydrogenase. Potential active-site cysteine and histidine residues were also indicated by the comparisons. The *sdhC* (384 bp) and *sdhD* (342 bp) structural genes encode 2 strongly hydrophobic proteins of 14,167 and 12,792 mol. wt., resp.. These proteins resemble in size and compn., but not sequence, the membrane anchor proteins of fumarate reductase (the *frdC* and *frdD* gene products).

IT 92941-88-3

NL PRO (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 92941-88-3 CAPLUS

CN DNA (Escherichia coli gene *sdhC*) (9CI) (CA INDEX NAME)

NTE double-stranded

SEQ 1 atgataagaa atgtaaaaaa acaaagacct gttaatctgg acctacagac
51 catccgggttc cccatcacgg cgatagcgtc catttccat cgcgtttccg
101 gtgtgatcac ctttgttgcg gtgggcattc tgcttggtct tctgggtacc
151 agcctctttt ccctgtaaagg ttgcagcaa gcttccgcga ttatggcag
201 ctttccgtc aaatttatca tgggggcatt ctttaccgct ctggcgatc
251 atgtcgatcg aggtattcgc cacatgtatg tggatttgg ctatctggaa
301 gaaacattcg aaggggtaa acgtccgcgaa aaaaatctct ttgttattac
351 tgtcgatcg tcaatttcgtc caggagccct cgtatggtaa

L65 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:133583 CAPLUS

DN 100:133583

TI Cloning vectors for expression of exogenous protein

IN Mayne, Nancy Gail; Burnett, James Paul, Jr.; Belegaje, Ramamoorthy; Hsiung, Hansen Maxwell

PA Eli Lilly and Co., USA

SO Eur. Pat. Appl., 61 pp.

CODEN: EPXXDW

DT Patent

STN Columbus

LA English

FAN, CNT 2

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|----------------|------|----------|-----------------|--------------|
| PI | EP 95361 | A1 | 19831130 | EP 1983-302935 | 19830523 <-- |
| | EP 95361 | B1 | 19890726 | | |
| R: BE, CH, DE, FR, GB, IT, LI, LU, NL, SE | | | | | |
| | IL 68753 | A1 | 19890131 | IL 1983-68753 | 19830522 |
| | GB 2121054 | A1 | 19831214 | GB 1983-14183 | 19830523 <-- |
| | GB 2121054 | B2 | 19860226 | | |
| | DK 8302306 | A | 19831126 | DK 1983-2306 | 19830524 <-- |
| | AU 8314912 | A1 | 19831201 | AU 1983-14912 | 19830524 <-- |
| | AU 560965 | B2 | 19870430 | | |
| | JP 58219199 | A2 | 19831220 | JP 1983-92197 | 19830524 <-- |
| | JP 07059193 | B4 | 19950628 | | |
| | DD 210306 | A5 | 19840606 | DD 1983-251214 | 19830524 <-- |
| | CA 1231068 | A1 | 19880105 | CA 1983-428700 | 19830524 |
| | JP 06073096 | A2 | 19940315 | JP 1992-351893 | 19920917 |
| PRAI | US 1982-381992 | A | 19820525 | | |
| | US 1982-382051 | A | 19820525 | | |

AB US 1982-382051 A 1982-382051
A recombinant DNA cloning vector is constructed by ligating (a) a replication origin, (b) a selection marker gene (gene for ampicillin resistance), (c) and an in-tandem DNA sequence comprising a promoter for a lipoprotein control sequence, the 5' untranslated region of a lipoprotein expression-control sequence (lpp gene from a gram-neg. bacterium), and a start codon that is followed immediately by a sequence coding for an exogenous protein or by a sequence coding for an enterokinase [89382-91-2] cleavage site to which is immediately joined a sequence

coding for an exogenous protein. When used as a cloning vector the lpp sequences control expression of exogenous DNA, but a nonhybrid protein product is formed; i.e. the translation product comprises methionine-optionally an enterokinase cleavage site-exogenous protein. Treatment with enterokinase removes the methionyl residue and leaves mature exogenous protein. Thus, to a plasmid contg. the Escherichia coli lipoprotein expression control sequence and plasmid pBR322 ampicillin-resistance genes was ligated a human growth hormone [12629-01-5] coding region with the use of a synthetic double-stranded DNA fragment complementary at 1 end to the natural lpp gene sequence (from the tbaI site through the initiating methionine codon), and at the other end, to the 1st 47 nucleotides of the gene for human growth hormone. The plasmid obtained, pNM645, was cloned in E. coli, and methionyl human growth hormone [82030-87-3] expression was verified by radioimmunoassay. The protein transcript represented 40% of the total protein with a yield of 22 million mols./cell. Biol. activity of the methionyl growth hormone with respect to proximal epiphyseal cartilage width in hypophysectomized female rats was the same as that of human growth hormone from cadavers.

IT 89382-91-2P

RL: PREP (Preparation)
 (prepn. cf. cattle growth hormone plasmid cloning vector construction
 in relation to)

RN 89382-91-2 CAPLUS

CN DNA, d(C-G-G-A-C-A-A-G-G-A-C-A-T-G-G-C-T-G-G-G-A-A-C-T-T-A-T-C-A-T-C-A-T-C-A-T-C-A-T-C-C-A-T-C-C-A-A-T-G-G-G-A-A-C-A-T-T-A-T-T-A-A-T-A-C-C-C-T), complex with DNA d(C-T-A-G-A-G-G-G-T-A-T-T-A-A-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-G-C-C-A-T-G-T-C-C-T-T-G-T-C) (1:1) (9CI) (CA INDEX NAME)

STRUCTURE DIAGRAM IS NOT AVAILABLE

29382-93-4P

PL: PREP (Preparation)

STN Columbus

(prep. of, human growth hormone plasmid cloning vector construction in relation to)

RN 89382-93-4 CAPLUS
CN DNA, d(C-T-A-G-A-G-G-T-A-T-T-A-A-T-G-T-T-C-C-C-A-T-T-G-G-A-T-G-A-T-G-A-T-G-A-T-A-A-G-T-T-C-C-C-A-A-C-C-A-T-T-C-C-C-T-T-A-T-C-C-A-G-G-C-T-T-T-G-A-C-A-A-C-G-C-T-A-T-G-C-T-C-C-G), complex with DNA
d(C-G-G-A-G-C-A-T-A-G-C-G-T-T-G-T-C-A-A-A-G-C-C-T-G-G-A-T-A-A-G-G-A-A-T-G-G-T-T-G-G-A-A-C-T-T-C-A-T-C-C-A-A-T-G-G-G-A-C-A-T-T-A-T-A-A-T-A-C-C-C-T) (1:1) (9CI) (CA INDEX NAME)

NTE doublestranded (2)

SEQ 1 ctagaggta ttaataatgt tcccattgga tgatgatgat aagttcccaa
51 ccattccctt atccaggctt ttggacaacg ctatgcctcg

1 cggagcatacg cggttgtcaaa aagcctggat aaggaaatgg ttgggaactt
51 atcatcatca tccaatggga acattattaa tacccct

L65 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1983:120463 CAPLUS

DN 98:120463

TI Promoter mapping and DNA sequencing of the F plasmid transfer genes traM and traJ

AU Thomson, Russell; Taylor, Linda

CS Inst. Virol., Univ. Glasgow, Glasgow, G11 5JR, UK

SO Molecular and General Genetics (1982), 188(3), 513-18

=====

CODEP: MGGEAE; ISSN: 0026-8925

DT Journal

LA English

AB The nucleotide sequence of the DNA encoding the traM and finP genes as well as the promoter proximal segment of the traJ gene of the F plasmid was detd. The predicted amino acid sequence for the traM protein shows that this inner-membrane protein has no signal sequence. The promoters for both the traM and traJ genes were mapped by in vitro transcription and nuclease S1 protection expts. No unambiguous location can be assigned to the finP gene, but all candidates, if translated, would encode small proteins of between 24 and 52 amino acids.

IT 85030-89-3

RL: PRP (Properties); BIOL (Biological study)

(nucleotide sequence of)

PN 85030-89-3 CAPLUS

CN DNA (plasmid F gene traM) (9CI) (CA INDEX NAME)

NTE doublestranded

SEQ 1 atggctaagg tgaacctgta tatcagcaat gatgcctatg aaaaaataaa
51 tgcgattatt gagaagcgctc gacaggaagg ggcaaggaa aaagatgtca
101 gtttttcagc aacagcttca atgcttcttg aactggggct tcgtgtacat
151 gagggctcaga tggagcgtaa agagtctgca tttaatcaga ctgagtttaa
201 taaaattgtttt cttgaatgcg ttgtaaaaac acaatcatca gttagcgaaaa
251 ttttgggtat tgagtctctc agtcctcatg tctccggaaa ttcaaagttt
301 gaataatgcca atatggttga agatatcagg gagaaggtat catctgagat
351 ggaacgattt ttccaaaaaa atgatgatga ataa

STN Columbus

L65 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982:401504 CAPLUS

DN 97:1504

TI The two yeast histone H2A genes encode similar protein subtypes

AU Choe, Joonho; Kolodrubetz, David; Grunstein, Michael

CS Mol. Biol. Inst., Univ. California, Los Angeles, CA, 90024, USA

SO Proceedings of the National Academy of Sciences of the United States of America (1982), 79(5), 1484-7

====

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The sequences of the 2 histone H2A genes in *Saccharomyces cerevisiae* were detd. These genes encode 2 histone H2A subtypes which are 131 amino acids in length but differ at 2 amino acid positions: an alanine → threonine and threonine → alanine change at positions 124 and 125. Thus, the 2 histone H2A subtypes have identical amino acid compns. The coding regions of the two H2A genes are homologous at 369 of 393 bases (94%), with all but 2 of the 24 changes being silent. There is only 30% homol. in the 5' flanking sequences of the two H2A genes. Like other eukaryotic histone genes, the yeast H2A genes are not interrupted by intervening sequences. When the yeast H2A histones are compared to those from other eukaryotes, there is ≥80% homol. in amino acid sequence.

IT 82029-65-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 32029-65-0 CAPLUS

CN DNA (*Saccharomyces cerevisiae* histone H2A2 gene) (9CI) (CA INDEX NAME)

NTE: double stranded

SEQ 1 atgtccggtg gtaaagggtgg taaagctgg tcagctgcta aagcttctca
 51 atctagatct gctaaagctg gtttaacatt cccagtgggt agagtgcaca
 101 gattgttaag aagaggtaac tacgcccaga gaattgggtc tgggtgctcca
 151 gtctatctga ctgctgtctt agaatatttg gctgctgaaa tttagaatt
 201 ggctggtaat gctgctagag ataacaaaaa aaccagaatt attccaagac
 251 atttacaatt ggcacatcaga aatgatgtg aattgaacaa gctattgggt
 301 aatgttacca tcgccccaaagg tggtgttttgc ccaaacattc accaaaactc
 351 gttgccaaag aagtctgcca agactgccaa agcttctcaa gaactgtaa

L65 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1982:16954 CAPLUS

DN 96:16954

TI Deoxynucleotide linkers to be attached to a cloned DNA coding sequence

IN Rutter, William J.

PA University of California, Berkeley, USA

SO Eur. Pat. Appl., 41 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN:CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|----|------------|------|----------|-----------------|--------------|
| PI | EP 35384 | A2 | 19810909 | EP 1981-300826 | 19810227 <-- |
| | EP 35384 | A3 | 19820908 | | |
| | EP 35384 | B1 | 19870610 | | |

R: BE, CH, DE, FR, GB, IT, NL, SE

STN Columbus

| | | | | |
|---------------------|----|----------|----------------|--------------|
| CA 1200773 | A1 | 19860218 | CA 1981-371674 | 19810225 <-- |
| ZA 8101308 | A | 19820331 | ZA 1981-1308 | 19810226 <-- |
| DK 8100888 | A | 19810830 | DK 1981-888 | 19810227 <-- |
| DK 166784 | B1 | 19930712 | | |
| AU 8167922 | A1 | 19810903 | AU 1981-67922 | 19810227 <-- |
| AU 545394 | B2 | 19850711 | | |
| JP 56166200 | A2 | 19811221 | JP 1981-29294 | 19810228 <-- |
| JP 06069375 | B4 | 19940907 | | |
| IL 62237 | A1 | 19850630 | IL 1981-62237 | 19810301 <-- |
| IL 71789 | A1 | 19850630 | IL 1981-71789 | 19810301 <-- |
| IL 71790 | A1 | 19850630 | IL 1981-71790 | 19810301 <-- |
| IL 71791 | A1 | 19850630 | IL 1981-71791 | 19810301 <-- |
| US 4769326 | A | 19880906 | US 1984-599464 | 19840412 |
| CA 1200774 | A2 | 19860218 | CA 1984-452925 | 19840426 <-- |
| CA 1200775 | A2 | 19860218 | CA 1984-452926 | 19840426 <-- |
| CA 1201075 | A2 | 19860225 | CA 1984-452927 | 19840426 <-- |
| PRAI US 1980-125878 | A | 19800229 | | |
| CA 1981-371674 | A3 | 19810225 | | |
| IL 1981-62237 | A | 19810301 | | |
| US 1982-403405 | A1 | 19820720 | | |

AB Specific oligonucleotide segments are prep'd. and linked to a cloned DNA coding segment in sequence which confer desired functional properties on the expression of the protein coded by the DNA coding sequence. Thus, the prepn. of a cloned human proinsulin gene and a specific cleavage linker is described, as well as the joining of the 2. The cloned DNA sequence coding for human proinsulin is isolated and prep'd., and the DNA linker sequence 5'-GATGATGATGATAAA-3' is chem. synthesized by the phosphotriester method of K. Itakura (1977). The linker sequence is blunt-end ligated to com. available HindIII linker which, when cleaved by HindIII endonuclease, yields a specific cleavage linker for insertion at a HindIII site. The product linker nucleotide sequences for both strands are AGCTTGGATGATGATGATAAA (plus strand) and ACCTACTACTACTATT (minus strand). The specific cleavage linker is blunt-end ligated with the cloned human proinsulin gene to produce a deoxynucleotide sequence of the plus strand contg. 5'-HindIII linker-specific cleavage linker-human proinsulin gene-3'.

IT 80208-71-5P
RL: SPN (Synthetic preparation); PREP (Preparation)
(prep'n. of, as translatable linker for mol. cloning)

RN 80208-71-5 CAPLUS

CN DNA, d(A-G-C-T-T-G-G-A-T-G-A-T-G-A-T-A-A-A) (9CI) (CA INDEX NAME)

SEQ 1 agcttggatg atgatgataa a

| | | |
|--|------------|---------|
| => file registry | SINCE FILE | TOTAL |
| COST IN U.S. DOLLARS | ENTRY | SESSION |
| FULL ESTIMATED COST | 90.86 | 786.46 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE | TOTAL |
| | ENTRY | SESSION |
| CA SUBSCRIBER PRICE | -8.03 | -22.63 |

FILE 'REGISTRY' ENTERED AT 17:47:08 ON 29 APR 2005
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Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9
DICTIONARY FILE UPDATES: 28 APR 2005 HIGHEST RN 849459-72-9

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when conducting SmartSELECT searches.

*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

```
=> s tgc(ccact/sqsn
L66    182547 TGCCCCACT/SQSN
=> s l66 and SQL<400
      23713436 SQL<400
L67    13495 L66 AND SQL<400
```

| | | |
|--|------------|---------|
| => file caplus | SINCE FILE | TOTAL |
| COST IN U.S. DOLLARS | ENTRY | SESSION |
| FULL ESTIMATED COST | 32.53 | 818.99 |
| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE | TOTAL |
| | ENTRY | SESSION |
| CA SUBSCRIBER PRICE | 0.00 | -22.63 |

FILE 'CAPLUS' ENTERED AT 17:47:56 ON 29 APR 2005
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STN Columbus

FILE COVERS 1907 - 29 Apr 2005 VOL 142 ISS 19
FILE LAST UPDATED: 28 Apr 2005 (20050428/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 167
L68 2432 L67

=> s 168 and PY<1987
11536051 PY<1987
L69 2 L68 AND PY<1987

=> d bib ab hitseq 1 2

L69 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2005 ACS or STN

Full Text

AN 1987:79507 CAPLUS
DN 106:79507
TI Sequences of liver cDNAs encoding two different mouse insulin-like growth factor I precursors
AU Bell, Graeme I.; Stempien, Michelle M.; Fong, Noel M.; Rall, Leslie R.
CS Chiron Corp., Emeryville, CA, 94608, USA
SO Nucleic Acids Research (1986), 14(20), 7873-82
CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB Some cDNAs encoding mouse liver insulin-like growth factor I (IGF-I) [67760-96-6] have been isolated and sequenced. Alternative RNA splicing results in the synthesis of two types of mouse IGF-I precursor that differ in the size and sequence of the COOH-terminal peptide. The sequences of the signal peptides, IGF-I moieties, and the first 16 amino acids of the COOH-terminal peptides or E-domains of the two precursors are identical. The sequence difference results from the presence in preproIGF-IB mRNA of a 52-base insertion which introduces a 17-amino acid segment into the COOH-terminal peptide of preproIGF-IB and also causes a shift in the reading frame of the mRNA. As a consequence of this insertion, the COOH-terminal 19 and 25 amino acids of mouse preproIGF-IA and -IB, resp., are different. The sequences of mouse and human preproIGF-IA are highly conserved and possess 94% identity. In contrast, the sequences of mouse and human preproIGF-IB are quite different in the region of the COOH-terminal peptide. A comparison of the sequences of mouse and human preproIGF-IB mRNA indicates that they are generated by different mol. mechanisms.

IP 106716-60-3

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 106716-60-3 CAPLUS

CN DNA (mouse clone migf1-2 insulin-like growth factor I cDNA) (9CI) (CA INDEX NAME)

NTE Double stranded

SEQ 1 atgtcgcttt cacaccttctt ctacacctggcg ctctgcttgc tcacacctcac
51 cagctccacc acagctggac cagagacacct ttgcggggct gagctgggtgg
101 atgctttca gttcgtgtgt ggaccggagg gcttttactt caacaagcccc
151 acaggtatcg gctccagcat tcggaggggca cctcagacag gcattgtggaa
201 ttagtgttgc ttccggagct gtatctttag gagactggag atgtactgtg
251 ccccaactgaa gcctacaaaaa gcagccccgt ctatccgtgc ccagcgccac
301 actgacatgc ccaagactca gaaggaagta catttgaaga acacaagtag

STN Columbus

351 aggaagtgcg ggaaacaaga cctacagaat gtag

L69 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2005 ACS on STN

Full Text

AN 1984:605219 CAPLUS

DN 101:205219

TI Cloning and sequencing of a sheep metallothionein cDNA

AU Peterson, M. Gregory; Lazdins, Ieva; Danks, David M.; Mercer, Julian F. B.

CS Birth Defects Res. Inst., R. Child. Hosp., Parkville, Australia

SO European Journal of Biochemistry (1984), 143(3), 507-11

=====

CODEN: EJBCAI; ISSN: 0014-2956

DT Journal

LA English

AB A partially purified metallothionein mRNA fraction from Cu-injected sheep liver was used to synthesize double-stranded cDNA, which was dC-tailed, annealed to dG-tailed plasmid pBR322, and used to transform Escherichia coli MC1061. Of 1500 recombinant clones, only 1 gave a pos. signal when screened with a mouse metallothionein 1 probe. This clone (pSMT-1) contained an insert which included the entire coding region of a sheep metallothionein, the whole 3'-untranslated region, part of the poly(A)-tail, and 25 bases of the 5'-untranslated region. DNA sequence anal. showed that this sheep metallothionein was very similar to other mammalian metallothioneins, except for a threonine to proline change at amino acid 27. The clone also contained a different polyadenylation signal d(A-G-T-A-A-A) from that usually found d(A-A-T-A-A-A). A comparison of the DNA sequence of the sheep metallothionein with those of other species revealed an interesting region of homol. close to the poly(A) addn. signal in the 3'-untranslated region of the mRNA.

IT 92942-24-0

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 92942-24-0 CAPLUS

CN DNA (sheep clone pSMT-1 metallothionein cDNA) (9CI) (CA INDEX NAME)

MTE doublestranded

SEQ 1 atggaccgcg actgtccctg ccccactggc ggctccgtca gctgcgtgg
51 ctcctgcacc tgcaggccct gcagatgcc ctccctgcaag aagagctgt
101 gctttgtcg ccctgtggcc tggcccaagt gtgcccgagg ctgtgtctgc
151 aaaggggccct cggacaagt cagctgtgc gcctga

=> d his; log y

(FILE 'HOME' ENTERED AT 16:55:34 ON 29 APR 2005)

FILE 'REGISTRY' ENTERED AT 16:56:02 ON 29 APR 2005

L1 O S TGCTTACAT/SQEN
L2 201666 S TGCTTACAT/SQSN
L3 14623 S L2 AND SQI<400

FILE 'REGISTRY' ENTERED AT 16:57:30 ON 29 APR 2005

L4 14623 S L3
L5 O S L4 AND PY<1987

STN Columbus

FILE 'CAPLUS' ENTERED AT 16:58:18 ON 29 APR 2005
L6 2668 S L3
L7 4 S L6 AND PY<1987

FILE 'STNGUIDE' ENTERED AT 17:00:49 ON 29 APR 2005

FILE 'REGISTRY' ENTERED AT 17:03:34 ON 29 APR 2005
L8 0 S CACTCATAT/SQEN
L9 157456 S CACTCATAT/SQSN
L10 9780 S L9 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:04:45 ON 29 APR 2005
L11 2154 S L10
L12 1 S L11 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:07:46 ON 29 APR 2005
L13 0 S GAAGGT CCT/SQEN
L14 193989 S GAAGGT CCT/SQSN
L15 16920 S L14 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:08:58 ON 29 APR 2005
L16 2703 S L15
L17 4 S L16 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:12:32 ON 29 APR 2005
L18 0 S GGGAGTACG/SQEN
L19 116522 S GGGAGTACG/SQSN
L20 5701 S L19 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:13:47 ON 29 APR 2005
L21 1154 S L20
L22 0 S L21 AND PY<1987
L23 0 S L21 AND PY<1988

FILE 'REGISTRY' ENTERED AT 17:14:20 ON 29 APR 2005
L24 0 S GGTATTGA/SQEN
L25 122237 S GGTATTGA/SQSN
L26 12580 S L25 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:15:34 ON 29 APR 2005
L27 2552 S L26
L28 1 S L27 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:17:25 ON 29 APR 2005
L29 0 S CAAGGGGCC/SQEN
L30 155151 S CAAGGGGCC/SQSN
L31 13136 S L30 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:18:38 ON 29 APR 2005
L32 2424 S L31
L33 1 S L32 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:20:30 ON 29 APR 2005
L34 0 S ACGGCAAGG/SQEN
L35 140454 S ACGGCAAGG/SQSN
L36 12155 S L35 AND SQL<400

FILE 'CAPLUS' ENTERED AT 17:21:41 ON 29 APR 2005
L37 2202 S L36
L38 3 S L37 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:25:55 ON 29 APR 2005

STN Columbus

L39 0 S CGTACATCG/SQEN
 L40 36728 S CGTACATCG/SQSN
 L41 4611 S L40 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:27:16 ON 29 APR 2005
 L42 769 S L41
 L43 2 S L42 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:30:53 ON 29 APR 2005
 L44 0 S GTCAGATCG/SQEN
 L45 57217 S GTCAGATCG/SQSN
 L46 5041 S L45 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:31:58 ON 29 APR 2005
 L47 1060 S L46
 L48 0 S L47 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:32:38 ON 29 APR 2005
 L49 0 S ATGAGGGCT/SQEN
 L50 161522 S ATGAGGGCT/SQSN
 L51 12306 S L50 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:33:33 ON 29 APR 2005
 L52 2438 S L51
 L53 2 S L52 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:35:59 ON 29 APR 2005
 L54 91301 S ATGAGCACG/SQSN
 L55 6980 S L54 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:36:50 ON 29 APR 2005
 L56 1660 S L55
 L57 2 S L55 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:38:57 ON 29 APR 2005
 L58 102811 S GGCCTGAAC/SQSN
 L59 11658 S L58 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:39:48 ON 29 APR 2005
 L60 1832 S L59
 L61 0 S L60 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:40:33 ON 29 APR 2005
 L62 603450 S ATGATGATG/SQSN
 L63 61649 S L62 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:41:18 ON 29 APR 2005
 L64 5122 S L63
 L65 11 S L64 AND PY<1987

FILE 'REGISTRY' ENTERED AT 17:47:08 ON 29 APR 2005
 L66 182547 S TGCCCCACT/SQSN
 L67 13495 S L66 AND SQL<400

FILE 'CPLUS' ENTERED AT 17:47:56 ON 29 APR 2005
 L68 2432 S L67
 L69 2 S L68 AND PY<1987

COST IN U.S. DOLLARS
 FULL ESTIMATED COST

SINCE FILE
 ENTRY
 18.24
 TOTAL
 SESSION
 837.23

STN Columbus

| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE
ENTRY | TOTAL
SESSION |
|--|---------------------|------------------|
| CA SUBSCRIBER PRICE | -1.46 | -24.09 |

STN INTERNATIONAL LOGOFF AT 17:49:39 ON 29 APR 2005

AN 1982:46833 CAPLUS
DN 96:46833
TI Regulation of the S10 ribosomal protein operon in E. coli: nucleotide sequence at the start of the operon
AU Olins, Peter O.; Nomura, Masayasu
CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA
SO Cell (Cambridge, MA, United States) (1981), 26(2, Pt. 2), 205-11
=====

CODEN: CELLB5; ISSN: 0092-8674

DT Journal

LA English

AB The DNA sequence of a 1250-base-pair segment of the Escherichia coli chromosome that carries the promoter for the S10 ribosomal protein operon, the S10 gene, and part of the L3 gene was detd. A DNA fragment carrying the putative S10 promoter was cloned into the plasmid mini-Col E1, which contains a transcription termination signal close to the single HindII site. Cells harboring the hybrid plasma produced a relatively stable hybrid mRNA with the expected sequence, demonstrating that the promoter functions in vivo. Comparison of the mRNA sequence around the start of the S10-coding region, the presumed target site for L4 repressor protein, with the known binding site for L4 on 23 S rRNA revealed the presence of sequence homologies. This supports the model of the translational feedback regulation of the S10 operon by L4.

IT 80451-23-6

RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

RN 80451-23-6 CAPLUS

CN DNA (Escherichia coli ribosome protein S 10 gene) (9CI) (CA INDEX NAME)

SEQ 1 atgcagaacc aaagaatccg tatccgcctg aaagcgtttgc atcatcggtct
51 gatcgatcaa gcaaccgcgg aaatcgctga gactgccaag cgcaactggtg
101 cgcagggtccg tggtccgatc ccgcgtccgaa cacgcaaaga gcgcttcact
151 gttctgtatct ccccgcacgt caacaaagac ggcgcgcgatc agtacgaaat
201 ccgtactcac ttgcgtctgg ttgacatcggt tgagccaaacc gagaaaaaccg
251 ttgatgtctct gatgcgtctg gatctggctg ccggtgtttaga cgtgcagatc
301 agcctgggtt aa

F161